STIC-Biotech/Cher	nLib	169	94	33	
From: Sent: CR	Chan, Christina Monday, October 24, 2005 5:39 PM Walicka, Malgorzata; STIC-Biotech/ChemLib	4.4	:	J. p.	;··

Please rush. Thanks

Chris Chan

Subject:

TC 1600 New Hire Training Coordinator and SPE 1644 (571)-272-0841 Remsen, 3E89

RE:

-----Original Message-----

From:

Walicka, Malgorzata

Sent:

Monday, October 24, 2005 3:50 PM

To:

Chan, Christina

Subject:

Christina, please authorize rush search of 3 short popeptides of SEQ ID NO:2, 3, and 9 in application 09/774,954. Please also against DNA data bases. Thank you.

Malgorzata

Malgorzata A. Walicka, Ph.D. Patent Examiner Art Unit 1652, Recombinant Enzymes USPTO, Remsen Building, Room 2C76 400 Dulany St. Alexandria, VA 22313 Mail Room 2C70 Tel. (571) 272-0944, fax (571) 273-0944 200 365 3 61 900 61

1118

Searcher: ______
Searcher Phone: ______
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search

NA#______ AA#:_____

S/L:____ Oligomer:_____

Encode/Transl:_____

Structure #:____ Text:___

Inventor:____ Litigation:___

/en	dors and cost where applicable
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	QUESTEL/ORBIT:
	LEXIS/NEXIS:
	SEQUENCE SYSTEM:
	WWW/Internet:
	Other (Specify):

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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

October 25, 2005, 15:21:23 Run on:

; Search time 210.606 Seconds (without alignments) 887.482 Million cell updates/sec

Title: Perfect score:

US-09-774-954-2 1979 1 MPAGSWDPAGYLLYCPCMGR......QGRPSSFFGWDRPPKLRDEF 365 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

1612378 seqs, 512079187 residues Searched:

1612378 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	HUMAN 09h488 homo sapien	ANTR Q6ev69 pan t	07yre7 bos		0 Q6ev70 rattus nor		OUSE		4 Q8awb4 gallus gal	16 Q7yre6 bos taurus		Q6ev71	18 Q7t028 brachydanio	Q8axs8	Q70ag7	Q6ev65		065981	ROME Q9v6x7	Q868a7	77 Q7qhs7 anopheles		Q8msr1		AEEL Q18014			OFU1_CRIGR P83337 cricetulus		Actor
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4 4	Query Match	100.0	100.0	95.8	94.9	93.7	93.6	95.6	92.4	84.5	80.1	75.3	75.3	74.5	73.1	72.1	70.5	42.9	42.3	42.0	41.8	39.9	39.7	39.3	38.5	33.4	32.5	29.5	14.9	9.5	8.2
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ALIGNMENTS

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R. Schnerch A.S., Schein J.E., Johes R.A.,
R. Schnerch A.S., Schein J.E., Johes R.A.,
R. R. Generation and initial analysis of more than 15,000 full-length human CHARACTERIZATION.
MEDLINE=97175972; PubMed=9023546;
Wang Y., Lee G.F., Kelley R.F., Spellman M.W.;
Identification of a GDP-L-fucose:polypeptide fucosyltransferase and enzymatic addition of 0-linked fucose to EGF domains.";
enzymatic addition of 0-linked fucose to EGF domains.";
elycobiology 6:837-842(1996).
-!- FUNCTION: Catalyzes the reaction that attaches fucose through an 0-glycosidic linkage to a conserved serine or threonine residue in EGF domains.
-!- CATALYTIC ATTIVITY: Transfers an alpha-L-fucosyl residue from GDPcomparative analysis of human chromosome 20."; beta-L-fucose to the serine hydroxy group of a protein acceptor, Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002). Event=Alternative splicing; Named isoforms=2; SEQUENCE FROM N.A. (ISOFORM 2). "The DNA sequence and comparture 414:865-871(2001). PATHWAY: Glycosylation. -1- ALTERNATIVE PRODUCTS rissum=Brain;

OFUL PANTR STANDARD; PRT; 388 AA.
06EVG9;
25-OCT-2004 (Rel. 45, Created)
25-OCT-2004 (Rel. 45, Last sequence update)
25-OCT-2004 (Rel. 45, Last sequence update)
GDP-fucose protein O-fucosyltransferase 1 precursor (EC 2.4.1.221) 384 LRDEF 388 RESULT 2 OFUL PANTR 셤 ઠે a ò 유 ò 셤 ઠે B H H H H This SWISS-PROT entry is copyright. It is produced through a collaboration the Buropean the Swiss Institute of Bioinformatics and the EMBL outstation use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by an for setting in the entries requires a license agreement (See http://www.isb-sib.ch/announce/ Note=No experimental confirmation available,
Note=No experimental confirmation available,
IIISSUE SPECIFICITY: Highly expressed in heart, brain, placenta,
lung, liver, skeletal muscle, kidney and pancreas. IsoId=09H488-2; Sequence=VSP_001809; IsoId=09H488-1; Sequence=Displayed;

Name=2;

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R GO; GO:0005737; C:Cytoplasm; ISS.
R GO; GO:001737; C:Integral to Golgi membrane; NAS.
GO; GO:0046922; F:peptide-O-tucosyltransferase activity; TAS.
GO; GO:000779; P:notch sgnaling pathway; ISS.
R GO; GO:0045449; P:regulation of transcription; NAS.
R GO; GO:006445; P:regulation of transcription; NAS.
W Alternative splicing; Pucose metabolism; Glycoprotein; SignAL.
I 26
Potential; Transferase. -> RENHSCVTLLFPR (in isoform 2). N-linked (GlcNAc. . .) (Potential) Score 1979; DB 1; Length 388; Pred. No. 1.1e-160; Indels 3FACCCA434D02415 CRC64; , 0 0; Mismatches EMBL; AF375884; AAL09576.1; -. EMBL; D80002; BAA11497.2; -. EMBL; ALIZ1897, CAC16424.1; -.
EMBL; BC000582; AAH00582.1; -.
Genew, HGNC:14988; POFUT:1; -. 388 AA; 43955 MW; 100.08; 11 Similarity 100.0%; 365; Conservative 0 62 160 388 Local Similarity 62 160 182 CARBOHYD VARSPLIC SEQUENCE CARBOHYD Query Match 121 Matches ò 셤 à g à

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QQLFKGKVKVVSLKPEVAQVDLYILGQADHFIGNCVSSFTAFVKRERDLQGRFSSFFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chara, O., Nagase, T., Kikuno, R. and Nomura, N.

Direct Submission

Direct Submission

Direct Submission

1532-3, Yana, Kisarazu, Chiba 292-0812, Japan

(R-mail:cdnainfo@kazusa.or.jp, Tel:+81-438-52-3913)

On May 9, 2002 this sequence version replaced gi:1136419.
                                                                                                                                                                                                                                                                                                 Nagase, T., Seki, N., Ishikawa, K., Tanaka, A. and Nomura, N. Prediction of the coding sequences of unidentified human genes. V. The coding sequences of 40 new genes (KTAA0161-KIAA0200) deduced by analysis of cDNA clones from human cell line KG-1

DNA Res. 3 (1), 17-24 (1996)

Fel. 99. | 96.81124
1071 CGGGAGCGGGACCTCCAGGGGGGGCGTCTTTCTTCGGCATGGACAGGCCCCCTAAG 1130
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                            linear
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 5249)
Managi, Y., Shao,Lv., Shi,S., Harris,R.J., Spellman,M.W., Stanley,P.
Managi,Y., Shao,Lv., Shi,S., Harris,R.J., Spellman,M.W., Stanley,P.
Modification of epidermal growth factor-like repeats with O-fucose.
Molecular cloning and expression of a novel GDP-fucose protein
O-fucosyltransferase
J. Biol. Chem. 276 (43), 40338-40345 (2001)
                              AF375884 5249 bp mRNA linear PRI 23-OCT-2001
Homo sapiens protein o-fucosyltransferase (POFUT1) mRNA, complete
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Submitted (02-MAY-2001) Cell Biology, Albert Einstein College of Submitted (02-MAY-2001) Cell Biology, Albert Einstein College of Medicine, 1300 Morris Park Ave., New York, NY 10461, USA
Location/Qualifiers
1. 5249
| / organism="Homo sapiens" / mol_type="mRNA" / db xref="texon:9606" / chromosome="20" / chromosome="20" / chromosome="20"
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2 (bases 1 to 5249)
Shi,S., Stanley,P., Wang,Y., Shao,L., Harris,R.J., Spellman,M.W. and Haltiwanger,R.S.
LysGlyLysValLysValValSerLeuLysProGluValAlaGlnValAspLeuTyrIle
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Q6ev70 rattus norv
Q7yrz3 sus scrofa
Q91zw2 mus musculu
Q8c8r4 mus musculu
Q8awb4 gallus gall
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Q9W589 Q6EV55 Q6EV53 Q6EV54 Q6EV54 Q6EV56 Q7Z4N0 Q7Z4N0 Q7T1N6 Q7T1N6 Q6EV52 Q7TRR5 Q7TRR5 Q6EV52 Q7PRQ3 Q6EV52 Q7PRQ3 Q6EV52 Q7PRQ3 Q6EV52 Q7PRQ3 Q6EV52 Q7PRQ3 Q6EV52 Q7PRQ3 Q6EV52 Q7PRQ3 Q6EV52 Q7PRQ3 Q6EV52 Q7PRQ3 Q6EV52 Q7PRQ3 Q6EV52 Q7PRQ3 Q6EV52 Q7PRQ3 Q6EV52 Q7PRQ3 Q6EV52 Q7PRQ3 Q6EV52 Q7PRQ3 Q6EV52 Q7PRQ3 Q6EV52 Q7PRQ3 Q7	RT; 3 ence up tation tation (O-PucT raniata atarrhi FUNCTI 8 R.J.,	of a 21).	TISSUE=Bone marrow; MEDLINE=96281124; PubMed=8724849; MEDLINE=96281124; PubMed=8724849; MEDLINE=96281124; PubMed=8724849; The coding sequences of unide The
4 4 6 4 4 4 4 4 4 4 4 6 6 4 6 6 6 6 6 6	STANDARD; PR' 85; O9BW76; (Rel. 41, Created) (Rel. 41, Last seque! (Rel. 45, Last annot crotein O-fucosyltrannot crocsyltransferase) ((Synonyms=KIAA0180; (Human). (Human). (Human). (Human). (Annotesyltransferase) (6) (Human). (Synonyms=KIAA0180; (Synonyms=KIAA0180	ferage."; m. 276:40338-40345(2001) m. N.A. (ISOFORM 1). http://www.n.a.more.edu.com/m.o.expression-ready/m.o.expre	TISSUE=Bone marrow; Nagase T., Seki N., Ishikawa KI Nagase T., Seki N., Ishikawa KI "Prediction of the coding sequency and rounds sequences of 40 new get analysis of CDNA clones from human DNA Res. 3:17-24(1996). [40] SEQUENCE FROM N.A. MEDLINE=21638749; PubMed=11780052 Deloukas P., Matthews L.H., Ashur Jones M., Stavrides G., Almeida J Bailey J., Barlow K.F., Bates K.N Back O.P., Blard C.P., Blakey S Buck O.P., Blard C.P., Blakey S Buck D., Burrill W.D., Butler A.P. Chapman J.C., Clamp M., Clark G., Collson A., Coville G.J., Deedman Ellingcon A.G., Frankland J.A., F Grafham D.V., Griffiths C., Griff
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RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA MAY M.P. Kumberley A.M., King A., Sin, Gatecol K., Johnson C.W., Johnson D.,
RA MAIR N. Kumberley A.M., King A., Kinghte A., Laird G.K., Lawlor S.,
RA MAIR N. Leverhall M.A., Lidd C., Liddo D.M., Morell J.D.,
RA MAIR N. L. Wartin S.L. Ware Wang P. Milly M.D. C., Liddo D.M., Morell J.D.,
RA MAIR N. Scharfer A. Pacel R. Pacer T.A.V. Feek A.I.,
RA RICE C.M., Rose M.T., Scotelland S.R., Plumb R.W., Ramany H.,
RA RICE C.M., Rose M.T., Scotelland C., Steward C.A., Sulson J.E.,
RA Hace C.M., Rose M.T., Scotelland C., Steward C.A., Sulson J.E.,
RA Hace C.M., Rose M.T., Scotelland C., Steward C.A., Sulson J.E.,
RA Hace C.M., Rose M.T., Scotelland C., Steward C.A., Sulson J.E.,
RA Hace C.M., Rose M.T., Scotelland C., Steward C.A., Sulson J.E.,
RA Hace C.M., Rose M. M. Habbard I.D., Williams D.W., Williams D.W., Williams D.W.,
Raumer R.M., Scotelland B.A., Grouse L.H., Bernelland C.P., Shank B. R.,
RA Manner R.D., Collins F. R., Scotelland C.C., Shank B. R.,
RA Alterdul S.F., Zeeberg B., Bueckow R.H., Shansen C.R., Schuler C.D.,
RA Alterdul S.F., Zeeberg B., Bueckow R.H., Shansen C.R., Schuler C.D.,
RA Alterdul S.F., Zeeberg B., Bueckow R.H., Shansen C.F., Bata B. R.,
RA Rausner R.D., Collins F.P., Zeeberg B., Boeckow R.H., Shansen R.D., Mullahy S.J.,
RA Rausner R.D., Coldins R.M., Gorden H.M., Garwitz T.L., Schemer C.R., Schuler P. H.,
RA Hans S., Loquelland N.A., Peters G.J., Marsann R.D., Mullahy S.J.,
RA Hans S., Loquelland N.A., Peters G.J., Marsann R.D., Mullahy S.J.,
RA Hans S., Loquelland N.A., Peters G.J., Marsann R.D., Mullahy S.J.,
RA Hanselly R.W., Manny D.W. Kornig A.C., Sharkin G.G.,
RA Manny W.R. Manny D.W. Kornig A.C., Sharkin G., Shalkin B.R.,
RA Hatenley R.W., Manny D.W. Schen B.J., Warns R.M.,
RA Hatenley R.W., Manny D.W. Schen B.J., Warns R.M.,
R.M. Manny Y. Lee G.F., Rallay R.P., Salaka L., Shanker C.C., Sharkin G., Shanker S.C.,
R.M. Manny Y. Lee G.F., Rallay R.R., Shalka L., Shanker C.C., Sharkin G.,
R.M. Schander A.C., Grim
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SVYVATDSESYVPELQQLFKGKVKVVSLKBEVAQVDLYILG
QADHFTGNCYSSFTAFVKRERDLQGRPSSFFGMDRPPKLRD
EP - REHNSCYTLLFPR (in isoform 2).
/PTIG=VSP 001809.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-linked (GlcNac. ..) (Potential).
N-linked (GlcNac. ..) (Potential).
NSTERPIVIALPCAPACETHRELOKYWNSDENVKTG
EAQTHRAHUNRYVGIHLRIGSDWKNACAMLKOGTAGSHFMA
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OFU1 PANTR STANDARD; PRT; 388 AA.

AC 068V69;
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last amocation update)
DF 25-OCT-2004 (Rel. 45, Last amocation update)
  EMBL; AF375884; AAL09576.1; -.

EMBL; AF275884; AAL09576.1; -.

EMBL; D80002; BAA11497.2; -.

EMBL; D80002; BAA11497.2; -.

EMBL; D80002; BAA11497.2; -.

EMBL; BC00582; AAR0582.1; -.

EMBL; BC00582; AAR0582.1; -.

R Genew; HGNC:14988; POFUTI.

R H: INVB; HIXO015724; -.

R GO, 200005737; C;cytoplasm; ISS.

GO; GO:0001737; C;cytoplasm; ISS.

GO; GO:0005721; P:embtyonic development; NAS.

R GO; GO:0005721; P:embtyonic development; NAS.

R GO; GO:0005721; P:embtyonic development; NAS.

R GO; GO:000521; P:egulation of transcription; NAS.

R GO; GO:0005449; P:regulation of transcription; NAS.

R GO; GO:0005445; P:regulation of translation; NAS.
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100.0%; Score 1979; DB 1; Length 388;
Best Local Similarity 100.0%; Pred. No. 1.1e-160;
Matches 365; Conservative 0; Mismatches 0; Indels 0;
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Bos taurus (Bovine)
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NCBI_TaxID=9913;
[1]
                                                                                                                                                                                                      NCBI_TaxID=9913;
                                                                                                                                      Name=pofut1;
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                                                                                                                                                                                                                                                                                                                                                                                         modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                          Glycobiology 13:IC-5C(2003).

-1- FUNCTION: Catalyzes the reaction that attaches fucose through an O-glycosidic linkage to a conserved serine or threonine residue in EGP domains (By similarity).

-1- CATALYTIC ACTIVITY: Transfers an alpha-L-fucosyl residue from GDP-beta-L-fucose to the serine hydroxy group of a protein acceptor.
-1- COFACTOR: Manganese (By similarity).
-1- PATHWAY: Glycosylation.
-1- SIMILARITY: Belongs to the glycosyltransferase 68 family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Potential.
GDP-fucose protein O-fucosyltransferase
                                                                                                                                                   "A new superfamily of protein-O-fucosyltransferases, alpha2-fucosyltransferases and alpha6-fucosyltransferases: phylogeny and identification of conserved peptide motifs.";
             Name-POFUT1; Synonyms-FUT12;
Pan troglodytes (Chimpanzee).
Bukaryota; Metazoa; Ghordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fucose metabolism; Glycoprotein; Glycosyltransferase; Manganese;
Signal; Transferase.
SIGNAL 1 26 Potential.
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160 160 N-linked (GlcNAc. .) (Potential)
388 AA, 43955 MW, 3FACCCA434D02415 CRC64;
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                                                                                             SEQUENCE FROM N.A.
PubMed=12966037; DOI=10.1093/Glycob/cwg113;
Martinez-Duncker I., Mollicone R., Candeller J.J., Breton C.,
(Peptide O-fucosyltransferase) (O-FucT-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AJ781500; CAH03712.1; -
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Matches 365; Conservative
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                                                        Mammalia; Euther
NCBI_TaxID=9598;
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207 EHRPLOKYMVWSDEMVRTGEAQIHAHLIRPYVGIHLRIGSDWKNACAMLKDGTAGAHFMA 266
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                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AY244580; AAQ02332.1; -.
GO; GO:0016757; F:transferase activity, transferring glycosyl. . .; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 SPOCYGYSRSTAAPLTWTWCLPDLKEIQRAVKLWVRSLDAQSVYVATDSESYVPELQQLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 HVSYQKYFKLEPLQAYHRVISLEDFMEKLAPTHWPPEKRVAYCFEVAAQRSPDKKTCPMK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MPAGSWDPAGYLLYCPCMGRFGNQADHFLGSLAFAKLLNRTLAVPPWIEYQHHKPPFTNL
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                                                                                                                                                                                                   Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 391;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7; Indels
                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
Loriol C., Germot A., Dupuy F., Maftah A.;
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44307 MW; 96762AB81A2027AD CRC64;
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25-0CT-2004 (TrEMBLrel. 28, Last sequence update)
25-0CT-2004 (TrEMBLrel. 28, Last annotation update)
Protein-0-fucosyltransferase 1.
                         QTXRE7;
1-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95.8%; Score 1895; DB 2; 93.4%; Pred. No. 1.8e-153; vative 17; Mismatches 7;
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                                                                                                                               Protein O-fucosyltransferase la.
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PRELIMINARY;
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RESULT 6
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                                                                                                                                                                                                                                                                                                                                                EGNPFGPFWDQFHVSFNKSELFTGISFSASYREQWSQRFSPKEHPVLALPGAPAQFPVLE 180
                                                                                                                                                                                                                                                                                                                                                                                               EHRPLOKYMVWSDEMVKTGEAQIHAHLVRPYVGIHLRIGSDWKNACAMLKDGTAGSHFMA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                            SPOCVGYSRSTAAPLTMTMCLPDLKEIQRAVKLWVRSLDAQSVYVATDSESYVPELQQLF 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KGKVKVVSLKPEVAQVDLYILGQADHFIGNCVSSFTAFVKRERDLQGRPSSFFGMDRPPK 360
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Eukaryota, Metazoa; Chordata; Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "A new superfamily of protein-O-fucosyltransferases, alpha2-fucosyltransferases and alpha6-fucosyltransferases: phylogeny and identification of conserved peptide motifs."; alpha913:15-56(2003):
                                                      "A new superfamily of protein-O-fucosyltransferases, alpha2-fucosyltransferases and alpha6-fucosyltransferases: phylogeny and identification of conserved peptide motifs."; conserved peptide jucification of conserved peptide motifs.";
                                                                                                                         Martinez-Duncker I., Oriol R., Mollicone R.;
Submitted (UTL-2004) to the BMBL/GenBank/DDBJ databases.
EMBL; AJ781503; CAH03714.1;
GO; GO:0016757; F:transferase activity, transferring glycosyl. Glycosyltransferase; Transferase activity, arangerase; Transferase; SEQUENCE 331 AA, 44277 MW; 4E047D6BBSCDF7FA CRC64;
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PubMed=12966037; DOI=10.1093/glycob/cwg113;
Martinez-Duncker I., Mollicone R., Candelier J.J., Breton C.
Oriol R.;
SEQUENCE FROM N.A.
PubMed=12966037; DOI=10.1093/glycob/cwgll3;
Martinez-Duncker I., Mollicone R., Candelier J.J., Breton C.,
Oriol R.,
                                                                                                                                                                                                          Length 391;
                                                                                                                                                                                                        Query Match
94.9%; Score 1878; DB 2; Length 3
Best Local Similarity 92.3%; Pred. No. 5e-152;
Matches 337; Conservative 20; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Protein-O-fucosyltransferase 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       395 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           124 PFGPFWDQFHVSFNKSELFTGISFSASYREQWSQRFSPKEHPVLALPGAPAQFPVLEEHR 183
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Martinez-Dunker I., Mollicone R., Candelier J.J., Breton C., Oriol R.;
Martinez-Dunker I., Mollicone R., Candelier J.J., Breton C., Oriol R.;
fucosyltransferases, and alpha6-fucosyltransferases: phylogeny and
identification of conserved peptide motifs.";
EMBL; AJ567917; CAD92201.1; -
GO; GO: 0016757; F.transferase activity, transferring glycosyl. . .; IEA-
GJycosylransferase; Transferase.
NON TER 178 378
SEQÜRNCE 378 AA; 42842 MW; 1870DEBOCSO713F1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 GSWDPAGYLLYCPCMGRFGNQADHFLGSLAFAKLLNRTLAVPPWIEYQHHKPPFTNLHVS 63
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Mammalia, Butheria, Cetartiodactyla, Suina, Suidae, Sus.
SEQUENCE FROM N.A.
STEALN-Wister
STRAIN-Wister
STRAIN-Wister
Martinez-Duncker I., Oriol R., Mollicone R.;
Martinez-Duncker I., Oriol R., Mollicone R.;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ781499; CAH03711.1;
GO; GO:0016757; P:transferase activity, transferring glycosyl.
GJycosyltransferase; Transferase activity, transferring glycosyl.
GJycosyltransferase; Transferase

Glycosyltransferase; Transferase

Glycosyltransferase; Transferase

Glycosyltransferase; Transferase

Glycosyltransferase; Transferase

Glycosyltransferase; Transferase

Glycosyltransferase

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
93.7%; Score 1854; DB 2; Length 395;
Best Local Similarity 94.2%; Pred, No. 5.7e-150;
Matches 341; Conservative 8; Mismatches 13; Indels
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MR-2004 (TrEMBLrel. 26, Last annotation update)
Protein-O-fucosyltransferase (Fragment)
Name=POFUI;
Sus Scrofa (Fig).
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93.6%; Pred. No. 6.6e-150;
tive 14; Mismatches 9;
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Best Local Similarity 93.6
Matches 336; Conservative
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STAIN=FVB/N-3; TISSUB=Mammary gland;
MEDINE=2238825; PubMed=1247932; DoI=10.1073/pnas.242603899;
MEDINE=2238825; PubMed=1247932; DoI=10.1073/pnas.242603899;
MA Strausberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,
Altschul S.F., Zeeberg B., Buetow K.H., Schnefer C.F., Bhate N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schnefer C.F., Bhate N.K.,
MA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heishe F.,
A stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.B.,
Brownstein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Brownstein M.J., Wokernan R.J., Marmannen P.H., Garzia A.M., Gasavant T.L., Schetz T.B.,
A stilaton D.K., Muzny D.M., Sodergren E.J., Lu X., Glibbs R.A.,
A villaton D.K., Muzny D.M., Sodergren E.J., Lu X., Glibbs R.A.,
A hiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Mhiting M., Madan A., Young A.C., Schmutz J., Myers R.M.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
B Schnerteibeld Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
M. Munich C. M., Schein J.E., Jones S.J.M., Marra M.A.;

Rad B. M., Schein J.E., Jones S.J.M., Marra M.A.;

Rad B. M., Schein J.E., Jones S.J.M., Marra M.A.;

Rad B. M., Schein J.E., Jones S.J.M., Marra M.A.;

Rad B. M., Marshars R. W.,

Rad B. M., Schein J.E., Jones E.D., Smailus D.E.,

Rad B. M., Marshars R. W.,

Rad B. M., M., Marshars R. W.,

Rad B. M., Marshars R
                                                                                                                                                                                                                        121 EGNPFGPFWDQFHVSFNKSELFTGISFSASYREQWSQRFSPKEHPVLALPGAPAQFPVLE 180
                                                                                                                                                                                                                                                           140 EGNPFGPFWDOFHVSFNKSELFAGISFSASYKDOWIORFSPKEHPVLALPGAPAQFPVLE 199
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                                                    79
                                   20 LPAVSWDPAGYLLYCPCMGRFGNQADHFLGSLAFAKLLNRTLAVPPWIEYQHHKPPFTNL
                                                                                                                                            80 HVSYQKYFKLEPLQVYHRVISLEDFMEKLAPTHWPPERRVAYCFEVAAQRSPDKKTCPMK
MPAGSWDPAGYLLYCPCMGRFGNQADHFLGSLAFAKLLNRTLAVPPWIEYQHHKPPFTNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21523965; PubMed=11524432; DOI=10.1074/jbc.M107849200; Wang Y., Shao L., Shi S., Harris R.J., Spellman M.W., Stanley P., Haltiwanger R.S.; "Modification of epidermal growth factor-like repeats with O-fucose: molecular cloning and expression of a novel GDP-fucose protein O-fucosyltransferase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q912W2;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
GDP-fucose protein 0-fucosyltransferase 1 precursor (EC 2.4.1.221)
(Peptide O-fucosyltransferase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentla; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J. Biol. Chem. 276:40338-40345(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=129/SvJ; TISSUE=Liver;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90
               -!- FUNCTION: Catalyzes the reaction that attaches fucose through an O-glycosidic linkage to a conserved serine or threonine residue in BGF domains (By similarity).
-!- CATALYTIC ACTIVITY: Transfers an alpha-L-fucosyl residue from GDP-beta-L-fucose to the serine hydroxy group of a protein acceptor.
-!- COFACTOR: Manganese (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           271 QCVGYSRSTATPLIMIMCLPDLKEIQRAVTLWVRALNARSVYIATDSESYVSEIQQLFKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 AGSWDPAGYLLYCPCMGRFGNQADHFLGSLAFAKLLNRTLAVPPWIEYQHHKPPFTNLHV
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GDP-fucose protein O-fucosyltransferase
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GO; GO:0030173; C:integral to Golgi membrane; ISS.
GO; GO:0008417; F:fucosyltransferase activity; ISS.
GO; GO:0001525; P:angiogenesis; IMP.
GO; GO:0007507; P:heart development; IMP.
GO; GO:0007399; P:neurogenesis; IMP.
GO; GO:0007399; P:neurogenesis; IMP.
GO; GO:0007419; P:O-linked glycosylation; ISS.
GO; GO:0001756; P:somitogenesis; IMP.
Fucose metabolism; Glycoprotein; Glycosyltransferase; Manganese;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67 67 N-linked (GlCNAC. . .) (Potential).
165 165 N-linked (GlCNAC. . .) (Potential).
393 AA; 44688 MW; D982104E95E5CF3B CRC64;
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                                                                                                                                            -!- SIMILARITY: Belongs to the glycosyltransferase 68 family.
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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4.3e-148;
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Best Local Similarity 92.6#
Matches 336; Conservative
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Signal; Transferase.
SIGNAL
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Best Local Similarity 92.34
Matches 335; Conservative
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SEQUENCE FROM N.A.

STAIN-C57BL/GJ; TISSUBE-Retina;
Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Adachi J., Aizawa K., Akimura T., Hara A., Hashizume W.,
A Hadashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
A Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
A Katch H., Kawai J., Kojima Y., Kondo S., Konno H., Konda M., Koya S.,
A Kurihara C., Matsuyama T., Miyazaki A., Murata M., Ohsato N., Okazumu A.,
A Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
A Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Taqami M.,
A Tagawa A., Takahashi F., Takaku-Akahiras S., Takeda Y., Tanaka T.,
Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE-Retina;
STRAIN=C57BL/6J; TISSUE-Retina;
BEDLINE-2409397; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
Furmanization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
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                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-C57BL/6J; TISSUE-Retina;
MEDLINE-99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Q8C8R4 PRELIMINARY; PRT; 393 AA.
01C8R4,
01CMAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Mus musculus adult relian cDNA, RIKEN [11]-length enriched library, clone:A930028F21 product:protein O-fucosyltransferase 1, full insert
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STRAIN-CSTBL/6J; TISSUE-Retina;
The FANTOM Consortium.
The RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I of II Team;
"Analysis of the mouse transcriptome based on functional annotation
60,770 full-length cDMSs";
Nature 420:563-573(2002).
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SEQUENCE FROM N.A.
STRAIN-CS7BL/G47 IISSUE-Retina;
MEDLINE-20510913; PubMed-11006861; DOI=10.1101/gr.152600;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Konno H., Akiyama J., Nishih K., Kitsunai T., Tashiro H., Itoh M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
Yangama Y., Ishikawa T., Cawa K., Tawak T., Matsuura S., Kawai J.,
Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.",
                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musimae; Mus
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STRAIN=CSPEL/6J; TISSUE=Retina;
STRAIN=CSPEL/6J; TISSUE=Retina;
MEDLINE=21085660;
RIKEN FANTOM COMSOCILIUM;
RIKEN FANTOM COMSOCILIUM;
"Functional annotation of a full-length mouse cDNA collection.";
"Agure 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                              Carninci P., Hayashizaki Y., "High-efficiency full-length cDNA cloning."; Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                 Name=Pofut1;
Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                 Length 393;
R MGD; MG12133207; Pofut1.

R GO; GO:0005615; C:extracellular space; TAS.

R GO; GO:00015615; P:andiogenesis; IMP.

R GO; GO:0001604; P:fucose metabolism; TAS.

R GO; GO:0007399; P:neurogenesis; IMP.

DR GO; GO:0007199; P:notrodesis; IMP.

DR GO; GO:0001719; P:notrodesis; IMP.

DR GO; GO:0001719; P:notrodesis; IMP.

R GO; GO:0001719; P:notrodesis; IMP.

R GO: GO:0001719; P:notrodesis; IMP.

R GIYCOSYILTANSferase; Transferase.

R GIYCOSYILTANSferase; Transferase.

R GIYCOSYILTANSferase; Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match

84.5%; Score 1672; DB 2; Length 3

Best Local Similarity 81.5%; Pred. No. 2e-134;

Matches 296; Conservative 33; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                             Indels
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Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ535754; CAD59738.1; -.
Hypotherical protein.
SEQUENCE 380 AA; 43316 MW; 83B53E342511811B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                           ; Score 1829; DB 2; 1; Pred. No. 7.8e-148; 14; Mismatches 14;
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KGKVKVVSLK---PEVAQVDLYILG
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Matches 261; Conservative
                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                  FROM N.A.
                                                                                                                                                                             NCBI_TaxID=8364;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Embryo;
Klein S., Gerh
                                                                                                                                                                                                             TISSUE=Embryo;
         301
                                                                                                                                                                                                 SEQUENCE
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                                                                                       Q640S0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPOCVGYSRSTAAPLTMTMCLPDLKEIQRAVKLWVRSLDAQSVYVATDSESYVPELQQLF 300
                                                                                                 242
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                                                                                                                                                   258 QCVGYDRSTAVPLTMDMCLPDLKEIKRALKVWVKKTVAKSIYIATDSEPYTKEIQQFFQG 317
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77
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Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY344581; AAQ02333.1; -.
EMBL; AY344581; P:transferase activity, transferring glycosyl. . .; IEA.
Glycosyltransferase; Transferase.
SEQUENCE 351 AA; 39576 MW; BF830F61A7296F42 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HVSYQKYPKLEPLQAYHRVISLEDFMEKLAPTHWPPEKRVAYCFEVAAQRSPDKKTCPMK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EGNPFGPFWDQFHVSFNKSELFTGISFSASYREQWSQRFSPKEHPVLALPGAPAQFPVLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EHRPLOKYMVWSDEMVKTGEAQIHAHLVRPYVGIHLRIGSDWKNACAMLKDGTAGSHFMA
                                                                                                            198 RPLHKYMVWSDEMVKKGEAYIHSLLVRPYVGIHLRIGSDWKNACNMLKDGTAGSHFMASP
                                                                                                                                                                                         1 MPAGSWDPAGYLLYCPCMGRFGNQADHFLGSLAFAKLLNRTLAVPPWIEYQHHKPPFTNL
                                                                     303 KVKVVSLKPEVAQVDLYILGQADHFIGNCVSSFTAFVKRERDLQGRPSSFFGMDRPPKLR
18 AGSWDTAGYLLYCPCMGRFGNQAEHFLGALAFARALNRTLAVPPWIEYRHHRPPYTNLHV
                   SYOKYFKLEPLQAYHRVISLEDFMEKLAPTHWPPEKRVAYCFEVAAQRSPDKKTCPMKEG
                             RPLOKYMVWSDEMVKTGEAQIHAHLVRPYVGIHLRIGSDWKNACAMLKDGTAGSHFMASP
                                                                                                                                        QCVGYSRSTAAPLTMTMCLPDLKEIQRAVKLWVRSLDAQSVYVATDSESYVPELQQLFKG
                                                          NPFGPFWDQFHVSFNKSELFTGISFSASYREQWSQRFSPKEHPVLALPGAPAQFPVLEEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                  Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
8
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                                                                                                                                                                                                                                                                                                                 01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Protein O-fucosyltransferase lb.
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                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                            DEF 380
                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                           Name=pofut1;
                                                                                                                                                                                                                                                                                                                                                                                                  Bovinae; Bos
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             126 GPFWDQFHVSFNKSELFTGISFSASYREQWSQRFSPKEHPVLALPGAPAQFPVLBEHRPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 WDSSGYILYCPCMGRFGNQADHFLGSLAFAKWYNRTLVVPPWIVYNHHRPPYTNVHVPYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66 KYPKLEPLQAYHRVISLEDFMEKLAPTHWPPEKRVAYCFEVAAQRSPDKKTCPMKEGNPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            186 QKYMVWSDEMVKTGEAQIHAHLVRPYVGIHLRIGSDWKNACAMLKDGTAGSHFMASPQCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 WDPAGYLLYCPCMGRFGNOADHFLGSLAFAKLINRTLAVPPWIEYQHHKPPFTNLHVSYQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein.

Kenopus tropicalis (Western clawed frog) (Silurana tropicalis).

Kenopus tropicalis (Western clawed frog) (Silurana tropicalis).

Kenopus tropicalis (Mestern Craniaca, Vertebrata, Euteleostomi, Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Kenopodinee; Kenopus.
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Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC082519; AAH82519.1; -.
Hypothetical protein.
SEQUENCE 380 AA; 43570 MW; 8BB938CE776D5238 CRC64;
                                                                                                                                                                                                                                                                                                                                                                              25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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; Pred. No. 7.2e-119;
48; Mismatches 50;
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PRT;
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Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBL_TaxID=7955;
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Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ51445; CAD55833.1; -.
InterPro; IPR000886; ER target_S.
PROSTIE; PS00014; ER TARGET; UNKNOWN_1.
Hypothetical protein. A 13505 WW; C6B960E76DB75293 CRC64;
                                                                                               Oriol R.;
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QBAXSB;
QDI-MAR-2003 (TYEMBLYEL: 23, Created)
O1-MAR-2003 (TYEMBLYEL: 23, LAST sequence update)
O1-MAR-2004 (TYEMBLYEL: 26, LAST annotation update)
Hypotherical protein pofut1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73.1%; Score 1447; DB 2;
70.6%; Pred. No. 3.4e-115;
tive 50; Mismatches 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          380 AA
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Matches 255; Conservative
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         261 GYDKYRAAPLTWEMCLPDLXEMRRALTLWVERSKARSVYIATDSTSHTEEIQAFLGDKVR 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     246 GYSRSTAAPLTWTWCLPDLKEIQRAVKLWVRSLDAQSVYVATDSESYVPELQQLFKGKVK 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65
                                                                     321 VVCLQPEVAQMDLYILGQADHFIGNCVSSFTAFVKRERDVHGRPSSFFGMDSPGAVQDE 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               306 VVSLKPEVAQVDLYILGQADHFIGNCVSSFTAFVKRERDLQGRPSSFFGMDRPPKLRDE 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   306 VVSLKPEVAQVDLYILGQADHFIGNCVSSFTAFVKRERDLOGRPSSFFGMDRPPKLRDE 364
                                                                                                                                                                                                                                                                                                                                                      Martinez Duncker I., Oriol R., Mollicone R.;
Submitted (UTL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ781498; CAH03710.1;
EMBL; AJ781498; CHRONJ310.1;
InterPro; IPR000886; ER target S.
PROSTIF; PRO10014; ET TARGET; UNKNOMN_I.
Glycosyltransferase; Transferase.
SEQUENCE 196 AA; 45056 MW; P90504E19507073F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 WDPAGYLLYCPCMGRFGNQADHFLGSLAFAKLLNRTLAVPPWIEYQHHKPPFTNLHVSYQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QKYMVWSDEMVKTGEAQIHAHLVRPYVGIHLRIGSDWKNACAMLKDGTAGSHFMASPQCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                       Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q7T028 PRELIMINARY; PRT; 395 AA.
Q7T028
Q7T0203 (TEMBLrel. 25, Created)
01-OCT-2003 (TEMBLrel. 25, Last sequence update)
01-OFT-2004 (TEMBLrel. 26, Last amnotation update)
01-MAR-2004 (TEMBLrel. 26, Last amnotation update)
DP-fucose protein O-fucosyltransferase 1 (EC 2.4.1.221).
Name-pofutl; Synonyms=futl2;
Name-pofutl; Synonyms=futl2;
Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota; Metazoa; Chordata; Craniata; Buteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 396;
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al Similarity 72.7%; Pred. No. 7.6e-119;
261; Conservative 48; Mismatches 50; Indels
                                                                                                                                                                                 25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Protein-O-fucosyltransferase.
                                                                                                                                                           Ä
                                                                                                                                                         396
                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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Best Local S
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                                                                                                                                                         Q6EV71
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077028
1D 07702
AC 07702
DT 01-0C
DT 01-0C
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
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ZFIN: ZDB-GREBE-0401039.2; pofcult of 200.00046922; F:peptide-O-fucosyltransferase activity; IEA.
GO; GO:0016757; F:transferase activity, transferring glycosyl.
Glycosyltransferase; Transferase activity, transferring glycosyl.
GLYCOSYLTRANSFERASE, TSPENSFERASE, T
SEQUENCE FROM N.A.
Martinez-Duncker I., Mollicone R., Candelier J.J., Breton C.,
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74.5%; Score 1474; DB 2; Length 395;
Best Local Similarity 73.9%; Pred. No. 1.8e-117;
Matches 263; Conservative 40; Mismatches 53; Indels
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                                                                                                                               139 PFGPFWDHFHVDFTQSELFDGITFSAYYKDVWISRFPPSQHPVIALPGAPAQFPVLEEHR 198
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19 GLYNSNGYIVYCPCMGRFGNQADHFLGSLAFAKMVNRTLVVPPWIVYNHHRPPYTNVHVP
                                                                                                           PFGPFWDQFHVSFNKSELFTGISFSASYREQWSQRFSPKEHPVLALPGAPAQFPVLEEHR
                                                YOKYFKLEPLOAYHRVISLEDFMEKLAPTHWPPEKRVAYCFEVAAORSPDKKTCPMKEGN
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Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
Butaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostem; Actinopterygii; Teleostei; Buteleostei; Neoteleostei; Acanthomorpha; Acanthomorpha; Acanthomorpha; Acanthomorpha; Acanthomorpha; Tetradontoidea; Tetradontidae; Takifugu.
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EMBL; AJG66070; CABLAJOS.1; E. Transferase activity, transferring glycosyl InterPro; IPR000886; ER target S. PROSITE; PS00014; ER TARGET; UKNOWN_I.
Glycosyltransferase; Transferase.
SEQUENCE 384 AA; 43650 MW; 7CAA6ADC90F40032 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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71.4%; Pred. No. 1.8e-113;
tive 43; Mismatches 59;
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Search completed: October 25, 2005, 15:35:23 Job time: 213.606 secs

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Sequence:

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AR163452 Sequence
BD103189 O-fucosyl
AR163451 Sequence
BD103188 O-fucosyl
AR32023 Homo sapi
DB6002 Homo sapi
DB6002 Homo sapi
AR780153 Sequence
BD103190 O-fucosyl
AY34650 Bos tauru
AJ78159 Rattus no
AJ781459 Rattus no
AJ567917 Sus scrof
AR163453 Sequence
BD103191 O-fucosyl
AR367955 Mus muscu
BC046295 Mus muscu
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AJ720352 Gallus ga
AJ744581 Bos tauru
BC082519 Xenopus t
AJ739536 Danio rer
AJ51425 Kenopus 1
AJ666070 Fugu rubr
AJ719585 Gallus ga
BC000582 Homo sapi
AK112708 Ciona int
AJ781502 Ciona say
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AY118651 Drosophil
AR50393 Sequence
CQ590403 Sequence
AB093572 Drosophil
CQ599402 Sequence
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Wang, Y. and Spellman, M.W.
O-fucosyltransferame
Patent: US 6270897-A 16 07-AUG-2001;
Location/Qualifiers
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Sequence 16 from patent US 6270987.
AR163457
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AJ606070
AJ781504
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/organism="unknown"
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AUTHORS
TITLE
JOURNAL
FEATURES
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AR163457
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       Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-MODEL=frame+ p2n.model -DEV=xlh
-Cen2_1/USPTO_spool_h/US09774954/runat_25102005_105432_6389/app_query.fasta_1.917
-D=-Cen2_1/USPTO_spool_h/US09774954/runat_25102005_105432_6389/app_query.fasta_1.917
-DE-CENZ_1/USPTO_spool_h/US09774954/runat_25102005_10-LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
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-NO_MMAP -LARREGOUERY -NEG-SCORES=0 -MAIT -DSPBICK=L10 -LONGLOG
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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BD103196 O-fucosyl
CQ727777 Sequence
AJ781500 Pan trogl
                                                                               October 26, 2005, 05:08:04; Search time 8270.58 Seconds (without alignments) 2138.440 Million cell updates/sec
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                GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                            - nucleic search, using frame_plus_p2n model
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Wang,Y. and Spellman,M.W.
O-fucosyltransferase
Patent: JP 2001527389-A 9 25-DEC-2001;
GENERTECH INC
OS Unidentified
N JP 2001527389-A/9
PD 25-DEC-2001
PF 31-DEC-1997 JP 19998532877
PR 31-DAN-1997 US 08/792498,26-NOV-1997 US
YANG WANG, MICHAEL W SPELLMAN
PC C12N15/54,C12N9/10,C07K16/40
CC Strandedness: Single;
CC Topology: Linear;
CC O-fucosyltransferase
FH Key
FT Source
1. 1100

FT 1. 1100

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Indels:
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Matches:
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Mismatches:
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Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. .
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PE Corporation (NY) (US)
Location/Qualifiers
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CQ727777
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AJ781500
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fut12 gene; pofut1 gene; protein-O-fucosyltransferase 1.
Pan troglodytes (chimpanzee)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                    321 LeuGlyGlnAlaAspHisPheIleGlyAsnCysValSerSerPheThrAlaPheValLys 340
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     910 CAGTCGGTCTACGTTGCTACTGATTCCGAGAGTTATGTGCCTGAGCTCCAACAGCTCTTC
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Unpublished
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/mol_type="mRNA"

/db_xref="taxon:9598"

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Submitted (06-7012-2004) Oriol R.,
Vaillant-Couturier, 94807, FRANCE
Location/Qualifiers
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/organism='Unidentified'
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Mismatches:
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Matches:
C12N15/54,C12N9/10,C07K16/40
Strandedness: Single;
Topology: Linear;
O-fucosyltransferase
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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                                              LeupheThrGly1leSerPheSerAlaSerTyzArgGluGlnTrpSerGlnArgPheSer
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25-DEC-2001
17-DEC-1997 JP 1998532877
31-JAN-1997 US 08/792498,26-NOV-1997 US
WANG,MICHAEL W SPELLMAN
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1 (bases 1 to 1514)
Wang, Y. and Spellman, M.W.
O-fucosyltransferase
Patent: JP 2001527389-A 1 25-DEC-2001;
GENBWTECH INC
OS Unidentified
PN JP 2001527389-A/1
PD 25-DEC-2001
PP 17-DEC-1997 JP 1998532877
PR 31-JAN-1997 US 08/792498, 26-NOV-1
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I (Dases i to 4560.)

Wambutt, R., Heubner, D., Mewes, H.W., Weil, B., Amid, C., Osanger, A., Pobo, G., Han, M. and Wiemann, S.

Incet Submission

Neulerberg, GERMAY.

Submitted (13-MAY-2003) MIPS, Ingolstaedter Landstr.1, D-85764

Neulerberg, GERMAY.

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Neulerberg, GERMAY.

Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing consortium of the German Genome Project.

This clone (DKFZ0451J114) is available at the RZPD in Berlin.

Please contact the RZED: Reseaucentrum, Heubnerweg 6, 14059

Berlin-Charlottenburg, GERMANY; Email: clone@tzpd.de Further information about the clone and the sequencing project is available at http://mips.gef.de/proj/CDNA/.

Incetion/Qualifiers

Inceticular (1450)
                                                                                                                                                                                                                                                                                                                        Homo sapiens mRNA; cDNA DKFZp451J114 (from clone DKFZp451J114).
AL832023.1 GI:21732563
                                                                                                                                                                                                                         961 CTCGGCCAAGCCGACCACTTTATTGCCAACTGTGTCTCCTCCTTCACTGCCTTTGTGAAG 1020
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                                                                                              841 CAGTCGGTCTACGTACTGATACCGAGAGTTATGTGCCCTGAGCTCCAACAGCTCTTC 900
                                                                                                                                                                           LeuGlyGlnAlaAspHisPheIleGlyAsnCysValSerSerPheThrAlaPheValLys 340
281 GlnSerValTyrValAlaThrAspSerGluSerTyrValProGluLeuGlnGlnLeuPhe 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="human skeletal muscle"
/clone_lib="451 (synonym: hlcc1). Vector pSport1; host
DH10B; Sites NotI + SalI"
/dev_stage="adult"
4538
                                  LeuProAspLeuLysGluIleGlnArgAlaValLysLeuTrpValArgSerLeuAspAla
                                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
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/mol_type="mRNA"
/db_xref="mxPD:DKF2451J114"
/db xref="taxon:9606"
/db capf="taxon:9606"
/clone="DKFZp451J114"
                                                                                                                                                                                                                                                                                      1081 CTGCGGGACGAGTTC 1095
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                                                                                         Conservative:
Mismatches:
Indels:
Gaps:
                                                              Length:
Matches:
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MORPPKLRDEF"
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Best Local Similarity:
Query Match:
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QKYFKLEPLQAYHRVISLEDFWEKLAPTHWPPEKRYAYCFEVAAQSESPDKKTCPWKEG
QKYFKLEPLQAYHRYSISLEFYGISFSASYREQWSQRFSPKEHPVLALPGAPAQFPVLE
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MASPQCYGYSRSTAPATTMYMCLPDLKEIQRAVKLWYSLDAQSVYVATDSESYVPEL
QQLFKGKVKVVSLKPEVAQVDLYILGQADHFIGNCVSSFTAFVKRERDLQGRPSSFFFG
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/db xref="GI:20521838"
/translation="PPRLCAAAGSGSRADMGAAAWARPLSVSFLLLLLPLPGMPAGSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (12-DEC-1995) Osamu Ohara, Kazusa DNA Research Institute, 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp, Tel:+81-438-52-3913) On May 9, 2002 this sequence version replaced gi:1136419.
1071 CGGGAGCGGGACCTCCAGGGGGGCCGTCTTTCTTCGGCATGGACAGGCCCCTAAG 1130
                                                                                                                                                                                                                                                                                                   Nagase, T., Seki, N., Ishikawa, K., Tanaka, A. and Nomura, N. Nagase, T., Seki, N., Ishikawa, K., Tanaka, A. and Nomura, N. The coding sequences of 40 new genes (KIAA0161-KIAA0200) deduced by analysis of cDNA clones from human cell line KG-1 BNA Res. 3 (1), 17-24 (1996) Feb. 96281124
                                                                                                                                                 PRI 10-JAN-2003
                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Chiang, P.W., Wang, S., Smithivas, P., Song, W.J., Ramamoorthy, S., Hillman, J., Puett, S., Van Keuren, M.L., Crombez, E., Kumar, A., Glover, T.W., Miller, D.B., Tsai, C.H., Blackburn, C.C., Chen, X.N., Sun, Z., Cheng, J.F., Korenberg, J.R. and Kurnit, D.M. Identification and analysis of the human and murine putative chromatin structure regulator Sup76H and Sup16h Genomics 34 (3), 328-333 (1996)
                                                                                                                                                 linear
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Ohara,O., Nagase,T., Kikuno,R. and Nomura,N.
Direct Submission
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/cell_line="KG-1"

/cell_type="myeloblast"

/tissue type="brain"

/clone_lib="pBluescriptII SK plus"
                                                                                                                                                             Homo sapiens KIAA0180 mRNA, complete cds
                                                                                                                                                   mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
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/gene="KIAA0180"
<1. .1213
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                                                                                   1131 Crecedaceacric 1145
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                                                  361 LeuArgAspGluPhe 365
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SerLeugluaspPheMetGluLysLeualaProThrHisTrpProProGluLysArgVal 100
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                                                                                                              1 MetProAlaGlySerTrpAspProAlaGlyTyrLeuLeuTyrCysProCysMetGlyArg
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Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                      US-09-774-954-2 (1-365) x AF375884 (1-5249)
  6.8e-174
1979.00
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Best Local Similarity:
Query Match:
DB:
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//imap="between PLAGL2 and KIF3B"
//issue_type="heart"
1. .5249
//gene="poFUT1"
//gene="poFUT1"
//function="catalyzes transfer of fucose from GDP-fucose to serine or threonine on epidermal growth factor-like
                                                                                                                                                                                                                                                                                                  Homo sapiens (human)
Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Eukaryota, Metazoa, Chordata, Catarrhini, Hominidae, Homo.

1 (bases 1 to 5249)
Mang, Y., Shao, L., Shi, S., Harris, R.J., Spellman, M.W., Stanley, P. and Haltiwanger, R.S.

Modification of epidermal growth factor-like repeats with O-fucose.
Molecular cloning and expression of a novel GDP-fucose protein
O-fucosyltransferase
J. Bhol. Chem. 276 (43), 40338-40345 (2001)
                                                  1016 AAAGGGAAGGTGAAGGTGAGCCGAAAGCCTGAAGCTGGACCCGAGGTCGACCTGTACATC 1075
                                                                                                                                                                                                                            AF375884 13-OCT-2001
Homo sapiens protein o-fucosyltransferase (POFUT1) mRNA, complete
    301 LysGlyLysValLysValValSerLeuLysProGluValAlaGlnValAspLeuTyrIle 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shi, S., Stenlary, P., Wang, Y., Shao, L., Harris, R.J., Spellman, M.W. Shi, S., Stenlary, P., Wang, Y., Shao, L., Harris, R.J., Spellman, M.W. and Haltiwanger, R.S.

Direct Submission
Submitted (OZ-MAY-201) Cell Biology, Albert Einstein College of Medicine, 1300 Morris Park Ave., New York, NY 10461, USA

Location/Qualifiers
1.5249
1.5249="MRNA"
// Corganism="Homo sapiens"
// Corganism="Homo sapiens"
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// College of Aref="Haxwa"
// Chromosome="20"
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AF375884.1 GI:15825113
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JP 2001527389-A/3
25-DEC-2001
17-DEC-1997 JP 1998532877
31-JAN-1997 JV 08/792498,26-NOV-1997 US
WANG, MICHAEL W SPELIMAN
C12N15/54,C12N9/10,C07K16/40
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Loors Wang, Y. and Spellman, M.W.

TITLE O-fucosyltransferase
JOURNAL Patent: JP 2001527389-A 3 25-DEC-2001;

GENENTECH INC
WHENT DP 2001527389-A/3
PD 25-DEC-2001
PP 17-DEC-1997 JP
PR 31-JAN-10°
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Dugas,M., Elis,R., Brors,B. and Mergenthaler,S.
Novel genetic markers for leukemias
Novel genetic markers for leukemias
10 Patent: WO 03039443-A 2310 15-WAY-2003;
Deutsches Krebsforschungszentrum (DE);
Ludwig-Maximilian-Universitaet Muenchen (DE); Haferlach, Torsten,
PD Dr. Dr. (DE); Schoch, Claudia (DE); Kern, Wolfgang (DE)
Location/Qualifiers

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                341 ArgGluArgAspLeuGlnGlyArgProSerSerPhePheGlyMetAspArgProProLys
                                                                             1139 CGGGAGCGGGACCTCCAGGGGAGGCCGTCTTTCTTCGGCATGGACAGGCCCCTAAG
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Matches:
Conservative:
Mismatches:
Indels:
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Best Local Similarity:
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Lorlol, C., Germot, A., Dupuy, F. and Maftah, A.
Genomic organization and expression profile of O-fucosyltransferase genes, pofutl and pofut2, in Bos taurus
Unpublished
2 (bases 1 to 1176)
                                                                          5075
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                                                                                                                                            5076 CAGTCGGTCTACGTTGCTACTGATTCCGAGAGTTATGTGCCTGAGCTCCAACAGGTCTTC 5135
                                                                                                                                                                                                                    AY344580 1176 bp mRNA linear MAM 03-AUG-2003
Bos taurus protein O-fucosyltransferase 1a (pofutl) mRNA, complete
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Submitted (17-JUL-2003) EA 3176 Glycobiologie et Biotechnologie,
Faculte des Sciences et Techniques, 123, Avenue A. Thomas, Limoges
                                                                                                                 300
                                                                                                                                                                                           301 LysGlyLysValLysValValSerLeuLysProGluValAlaGlnValAspLeuTyrile 320
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Bos taurus
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
Bovinae, Bos.
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1956 TCTCCGCAGTGTGTGGGCTACAGCCGCAGCACAGCGGCCCCCCCTCACGATGACTATGTGC
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AY344580.1 GI:33303529
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                                                                   ce 1. 11284 / Organism='Unidentified'.
Location/Qualifiers
                                                                                                                                                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                             Location/Qualifiers

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Strandedness: Single;
Topology: Linear;
O-fucosyltransferase
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1979.00
100.00%
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                                                             Key
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Best Local Similarity:
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MAM 07-JUL-2004 (fut12 gene).

Euteleostomi;

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/gene-
function="adds fucose to Ser or Thr"
/note="pofut1"
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                                                                                 1099 CGGGAACGGGACCTCCATGGGAGACCATCCTTCTTTGGCATGGACAGGCCCCCTCAG 1158
                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
                      LeuGlyGlnAlaAspHisPheIleGlyAsnCysValSerSerPheThrAlaPheValLys
                                                           ArgGluargAspLeuGlnGlyArgProSerSerPhePheGlyMetAspArgProProLys
                                                                                                                                                                                                                                                                                                                                               Martinez-Duncker, I., Mollicone, R., Candelier, J.J., Breton, C. Oriol, R.
A new superfamily of protein-O-fucosyltransferases, alpha2-fucosyltransferases; and alpha6-fucosyltransferases: phylogeny and identification of conserved peptide motifs (12966037)
                                                                                                                                                                                                                                        AJ781503.1 GI:50057075
fut12 gene; pofut1 gene; protein-O-fucosyltransferase
Bos taurus (cow)
Bos taurus
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                                                                                                                                                                                         1176 bp mRNA linear
Bos taurus mRNA for protein-O-fucosyltransferase 1
AJ781503
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Unpublished
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Matches:
Conservative:
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Indels:
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Submitted (06-7012-2004) Oriol R.,
Vaillant-Couturier, 94807, FRANCE
Location/Qualifiers
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DEFINITION
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AUTHORS
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AJ781503
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           Length:
Matches:
Conservative:
Mismatches:
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98.08%
93.42%
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Query Match:
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                                                       ThrLeuAlaValProProTrpIleGluTyrGlnHisHisLysProProPheThrAsnLeu
                                                                                  HisValSerTyrGlnLysTyrPheLysLeuGluProLeuGlnAlaTyrHisArgValIle
                                                                                                           MetProAlaGlySerTrpAspProAlaGlyTyrLeuLeuTyrCysProCysMetGlyArg
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Search completed: October 26, 2005, 12:55:24
Job time : 8300.58 secs
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LeuArgAspGluPhe 365
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winbatin (Geneticch)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/774,954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/09774954
Publication No. US20040241645A1
GENERAL INFORMATION:
APPLICANT: Yang Wang, Michael W. Spellman
TITLE OF INVENTION: O-Fucosyltransferase
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/978,741
FILING DATE: 26-NOV-1997
APPLICATION NUMBER: 08/792,498
FILING DATE: 31-JAN-1997
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36192, A
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Sequence 366, App
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                                                                                                                                       October 25, 2005, 15:22:39; Search time 214.353 Seconds (without alignments) 710.936 Million cell updates/sec
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                                                                                                                                                                                                                                       US-09-774-954-2
1979
1 MPAGSWDPAGYLLYCPCWGR......QGRPSSFFGWDRPPKLRDEF 365
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Sequence 6,
Sequence 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 8,
Sequence 9,
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Sequence 2
Sequence 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Coptodata/2/pubpaa/DST_NEW_PUB.ppp.;

6/ptodata/2/pubpaa/DST_NEW_PUB.ppp.;

6/ptodata/2/pubpaa/USO6_PUBCOMB.ppp.;

6/ptodata/2/pubpaa/USO6_PUBCOMB.ppp.;

6/ptodata/2/pubpaa/USO7_NEW_PUB.ppp.;

6/ptodata/2/pubpaa/USO8_PUBCOMB.ppp.;

6/ptodata/2/pubpaa/USO8_PUBCOMB.ppp.;

6/ptodata/2/pubpaa/USO9_PUBCOMB.ppp.;

6/ptodata/2/pubpaa/USO9_PUBCOMB.ppp.;

72/6/ptodata/2/pubpaa/USO9_PUBCOMB.ppp.;

73/6/ptodata/2/pubpaa/USO9_PUBCOMB.ppp.;

74/6/ptodata/2/pubpaa/USO9_PUBCOMB.ppp.;

75/ptodata/2/pubpaa/USO9_PUBCOMB.ppp.;

76/ptodata/2/pubpaa/USO9_PUBCOMB.ppp.;

76/ptodata/2/pubpaa/USO9_PUBCOMB.ppp.;

76/ptodata/2/pubpaa/USO0_PUBCOMB.ppp.;

76/ptodata/2/pubpaa/USO0_PUBCOMB.ppp.;

76/ptodata/2/pubpaa/USO0_PUBCOMB.ppp.;

76/ptodata/2/pubpaa/USO0_PUBCOMB.ppp.;

76/ptodata/2/pubpaa/USO0_PUBCOMB.ppp.;

76/ptodata/2/pubpaa/USO0_PUBCOMB.ppp.;

76/ptodata/2/pubpaa/USO0_PUBCOMB.ppp.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:
/cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:
/cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        prodata/2/pubpaa/US07_PUBCOMB.pep:
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-301-822-169 C
US-09-774-954-6 C
US-09-774-954-17 ·
US-11-097-143-18162
US-09-774-954-8
US-09-774-954-8
US-09-774-954-9
US-10-774-954-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                            1862994 segs, 417510619 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Published Applications AA:
                                                                                               OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                         BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Match Length DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                         Scoring table:
                                                                                                                                                                                                                                                                                              Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                               Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Database
                                                                                                                                                 Run on:
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ALIGNMENTS

ADDRESSEE: Genentech, Inc. STREET: 1 DNA Way CITY: South San Francisco STATE: California

COUNTRY: USA

NAME: Svoboda, Craig G. REGISTRATION NUMBER: 39,044 REFERENCE/DOCKET NUMBER: P1041P1

FILING DATE: 30-Jan-2001 CLASSIFICATION: <Unknown>

8, Appli 102, Appli 162078, 1621078, 328476, 65103, A 11, 3910, 11, 3910, 11, 3910, 1120, App 122, App 122, App 122, App 1321, A 1321, App 1321, App 13210, A 13210, A 13210, A 1426, App 16118, App	9
Sequence Seq	מיייי
10. 4.25. 11.45. 11.6. 1.6. 1.6. 1.6. 1.6. 1.6. 1.6. 1	- 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1
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180

203

120

83

240

263

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84 HVSYQKYFKLEPLQAYHRVISLEDFMEKLAPTHWPPEKRVAYCFEVAAQRSPDKKTCPMK 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301 KGKVKVVSLKPEVAQVDLYILGQADHFIGNCVSSFTAFVKRERDLQGRPSSFFGMDRPPK 360
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                                                                                                                                                                                                                                                             121 EGNPFGPFWDQFHVSFNKSELFTGISFSASYREQWSQRFSPKEHPVLALPGAPAQFPVLE
                                                                                                                                                                                                                                                                                                                                                       24 MPAGSWDFAGYLLYCPCMGRFGNQADHFLGSLAFAKLINRTLAVPBWIEYQHHKPPFTNL
                                                                                                                                                                                         61 HVSYQXYFYLLEPLQAYHRVISLEDFMEXLAPTHWPPEKRVAYCFEVAAQRSPDKXTCPMK
                                                                                                                                                                                                                                                                                                                                   EHRPLOKYMVWSDEMVKTGEAQIHAHLVRPYVGIHLRIGSDWKNACAMLKDGTAGSHFMA
                                                                                                                                                                                                                                                                                                                                                                                                       241 SPOCYGYSRSTAAPLTMTMCLPDLKEIQRAVKLWVRSLDAQSVYVATDSESYVPELQQLF
                                                                                                                     1 MPAGSWDPAGYLLYCPCMGRFGNQADHFLGSLAFAKLLNRTLAVPPWIEYQHHKPPFTNL
                                                                                   Gaps
                                             Query Match
100.0%; Score 1979; DB 14; Length 388;
Best Local Similarity 100.0%; Pred. No. 1.2e-195;
Matches 365; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READALE PORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER READALE PORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/774,954
FILING DATE: 30-Jan-2001
PRING DATE: 30-Jan-2001
PRING DATE: 31-JAN-1997
APPLICATION NUMBER: US/08/978,741
PILING DATE: 31-JAN-1997
ATORNEY/AGENT INFORMATION:
MAME: SYODOGA, CTABJG G,
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: 19041P1
TELECOMMUNICATION INFORMATION:
TELEBERORE 650/252-1489
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-US-1/14-594-6

Sequence 6, Application US/09714954

Sequence 6, Application No. US204041645A1

GENERAL INFORMATION:

APPLICANT: Yang Wang, Michael W. Spellman

TITLE OF INFORMATION: O-PUCOSYLITANSFERASE

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSE: Genentech, Inc.

STREET: 1 DNA WAY

CITY: South San Francisco

STATE: California
; ORGANISM: Homo Sapiens
US-10-301-822-169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 SPOCVGYSRSTAAPLTMTMCLPDLKEIQRAVKLWVRSLDAQSVYVATDSESYVPELQQLF 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPQCVGYSRSTAAPLIMIMCLPDLKEIQRAVKLWVRSLDAQSVYVATDSESYVPELQQUF 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KGKVKVVSLKPEVAQVDLYILGQADHFIGNCVSSFTAFVKRERDLQGRPSSFFGMDRPPK 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 HVSYQKYFKLEPLQAYHRVISLEDFMEKLAPTHWPPEKRVAYCFEVAAQRSPDKKTCPMK 120
                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                     1 MPAGSWDPAGYLLYCPCMGRFGNQADHFLGSLAFAKLLNRTLAVPPWIEYQHHKPPFTNL 60
                                                                                                                                                                                                                                                                                                                                                                                                                 121 EGNPFGPFWDQFHVSFNKSELFTGISFSASYREQWSQRFSPKEHPVLALPGAPAQFPVLE
                                                                                                                                                                                                                                                   1 MPAGSWDPAGYLLYCPCMGRFGNQADHFLGSLAFAKLLNRTLAVPPWIEYQHHKPPFTNL
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                                                                                                                                                                               Length 365;
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                                                                                                                                                                           Query Match
100.0%; Score 1979; DB 11;
Best Local Similarity 100.0%; Pred. No. 1.1e-195;
Matches 365; Conservative 0; Mismatches 0;
                                                                                         ;
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-774-954-2
 TELEPHONE: 650/225-1489

TELERAX: 650/952-981

TELERAX: 650/952-981

TELERAX: 650/952-981

TENGRATION FOR SEQ ID NO: 2:

LENGTH: 365 amino acids

TYPE: Amino Acid
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Gaps

202

262

322

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US-11-097-143-148162

Sequence 18162, Application US/11097143

Publication No. US200S0208558A1

GENERAL INFORMATION:

APPLICANT: Venter, J. Craig

APPLICANT: Venter, J. Craig

APPLICANT: Venter, J. Craig

TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID

TITLE OF INVENTION: DROSOPHILA GENES.

CURRENT APPLICATION NUMBER: US/11/097,143

CURRENT PILING DATE: 1999-10-05

PRIOR APPLICATION NUMBER: 60/160,191

PRIOR APPLICATION NUMBER: 60/160,191

PRIOR FILING DATE: 1999-11-12

PRIOR FILING DATE: 2000-02-24

PRIOR FILING DATE: 2000-02-24

PRIOR FILING DATE: 2000-03-23

NUMBER OF SEQ ID NOS: 43008

SOFTWARE: FEASTERQ FOR WINDOWS VERSION 4.0

LENGTH: 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 TGISFSASYREQWSQRFSPKEHPVLALPGAPAQFPVLEEHRPLQKYMVWSDEMVKTGEAQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 DLKEIQRAVKLIMVRSLDAQSVYVATDSESYVPELQQLFKGKVKVVSLKPEVAQVDLYILG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 EDFMEKLAPTHWPPEKRVAYCFEVAAQRSPDKKTCPMKEGNPFGPFWDQFHVSFNKSELF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 IHAHLVRPYVGIHLRIGSDWKNACAMLKDGTAGSHFWASPQCVGYSRSTAAPLTMIMCLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DLKEIQRAVKLWVRSLDAQSVYVATDSESYVPELQQLFKGKVKVVSLKPEVAQVDLYILG
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                                                                                                                                                                                                                                                         Length 343;
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                                                                                                                                                                                                                                                  Query Match
93.2%; Score 1844; DB 11;
Best Local Similarity 100.0%; Pred. No. 9.6e-182;
Matches 343; Conservative 0; Mismatches 0;
                                                                                                                 LENGTH: 343 amino acids
TYPE: Amino Acid
TYPE: Linear
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
TELECOMMUNICATION INFORMATION
                          TELEPHONE: 650/225-1489
TELEPAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-11-097-143-18162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     213 EHRPLOKYWVWSDEMVKTGEAQIHAHLVRPYVGIHLRIGSDWKNACAMLKDGTAGSHFMA 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 SPQCVGYSRSTAAPLTWITMCLPDLKEIQRAVKLWVRSLDAQSVYVATDSESYVPELQQLF 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EGNPFGPFWDQFHVSFNKSELFTGISFSASYREQWSQRFSPKEHPVLALPGAPAQFPVLE 180
                                                                                                                                                                                                                                                                                                         92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    273 SPQCVGYSRSTAAPLIMITMCLPDLKEIQRAVKLWYRSLDAGSVYVATDSESYVPELQQLF
                                                                                                                                                                                                                                                                                      1 MPAGSWDPAGYLLYCPCMGRFGNQADHFLGSLAFAKLLNRTLAVPPWIEYQHHKPPFTNL
                                                                                                                                                                                                                  Gaps
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0
                                                                                                                                                                  Query Match 100.0%; Score 1979; DB 11; Length 397; Best Local Similarity 100.0%; Pred. No. 1.3e-195; Matches 365; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/774,954
FILING DATE: 30-3an-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION: «Unknown»
PRIOR APPLICATION NUMBER: US/08/978,741
FILING DATE: 26-NOV-1997
APPLICATION NUMBER: 08/792,498
FILING DATE: 31-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 17, Application US/09774954
Publication No. US20040241645A1
GENERAL INFORMATION:
APPLICANT: Yang Wang, Michael W. Spellmar
TITLE OF INVENTION: O-Fucosyltransferase
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
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                                                            TOPOLOGY: Linear SEQ ID NO: 6: US-09-774-954-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: South San Francisco
STATE: California
COUNTRY: USA
                                 LENGTH: 397 amino acids TYPE: Amino Acid
              SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 361 LRDEF 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             393 LRDEF 397
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US-09-774-954-17
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Query Match
40.9%; Score 809; DB 11; Length 165;
Best Local Similarity 96.9%; Pred. No. 4.7e-75;
Matches 155; Conservative 0; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 474 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                          RESULT 7
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LOCATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (4)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
LOCATION: (5)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
NAME/KEY: SITE
NAME/KEY: SITE
NAME/KEY: SITE
LOCATION: (148)
COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
[15-09-833-245-366]
                                                                                                                    6
                                                                                                                                                                                                                                                                                                                              122 GNPFGPFWDOFHVSFNKSELFTGISFSASYREQ---WSQRFSPKEHPVLALPGAPAQFPV 178
                                                                                                                                                                                                                                                                                                                                                                   146 GNPFGPFWDTFHIDFVRSEFYAPLHFDVHHSNBAAKWQTKYPAESYPVLAFTGAPASFPV 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                        206 QLENCKLÖRYLOWSQRYREASKDFIREQLPRGAFLGIHLRNGIDWVRACEHVKD---SQH 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 179 LEEHRPLOKYMVWSDEMVKTGEAQIHAHLVR-PYVGIHLRIGSDWKNACAMLKDGTAGSH 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       238 FMASPOCVGYSRSTAAPLTWIMCLPDLKEIQRAVKLWVRSL-----DAQSVYVAIDSE 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 263 LFASPQCLGYKNERGA-LYPELCMPSKEAIIRQLKRTIKNVRQTQPDNEIKSVFVASDSN 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            291 SYVPELQ-QLFKGKVKVVSLKPEVAQVDLYILGQADHFIGNCVSSFTAFVKRERDLQGRP 349
                                                                                                                                                                                                                                                 67 YFKLEPLQAYHRVISLEDFMEKLAPTHWPPEKRVAYCFE----VAAORSPDKKTCPMKE 121
                                                                                                                                                                99
                                                                                                                                                                                     28 DPNGYLTYCPCMGRFGNQADHFLGSLAFAKALNRTLILPPWVEYR--RGELRSRQVPFNT 85
                                                                                                                                                              7 DPAGYLLYCPCMGRFGNQADHFLGSLAFAKLLNRTLAVPPWIEYOHHKPPFTNLHVSYQK
                                                                                                                       26; Gaps
                                                                             DB 20; Length 402;
                                                                        Query Match
42.0%; Score 831; DB 20; Length 402
Best Local Similarity 44.7%; Pred. No. 9e-77;
Matches 167; Conservative 62; Mismatches 119; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-833-245-366
US-09-833-245-366
Sequence 366, Application US/09833245
Sequence 366, Application US/09833245
Sequence 366, Application No. US20040010134A1
GENERAL INFORMATION:
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: FF546PCT
CURRENT APPLICATION NUMBER: US/09/833,245
CURRENT FILING DATE: 2001-04-12
PRIOR PILING DATE: 2000-04-12
PRIOR FILING DATE: 2000-04-12
PRIOR FILING DATE: 2000-12-21
PRIOR FILING DATE: 2000-12-21
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 2267
SEQ ID NOS: 2267
SEQ ID NOS: 2267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (2)
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-18162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              206 HLVRPYVGIHLRIGSDWKNACAMLKDGTAGSHFMASPQCVGYSRSTAAPLTMTMCLPDLK 265
                                                                                                                                                           266 EIQRAVKLWVRSLDAQSVYVATDSESYVPELQQLFKGKVKVVSLKPEVAQVDLYILGQAD 325
                                                                                                                                                                                     66 BIQRAVKIWVRSLDAQSVYVATDSESYVPBLQQLFKGKVKVVSLKPBVAQVDLYILGQAD 125
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                                                                                 6 HFARTYPGIHLRIGSDWKNACAMLKDGTAGSHFMASPQCVGYSRSTAAPLTWTMCLPDLK
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READALE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genetech)
CURRENT APPLICATION DATA:
APPLICATION NAMES: US/09/774,954
FILING DATE: 30-Jan-2001
CLASSIFICATION NUMBER: US/09/774,954
PILING DATE: 26-NOV-1997
APPLICATION NUMBER: 08/792,498
FILING DATE: 26-NOV-1997
APPLICATION NUMBER: 08/792,498
FILING DATE: 31-JAN-1997
APPLICATION NUMBER: 19,044
RESTRENCE/DOCKET NUMBER: 39,044
REGISTRATION NUMBER: 39,044
REGISTRATION NUMBER: 39,044
REGISTRATION NUMBER: 39,044
RESTRENCE/DOCKET NUMBER: 19101PI
TELEPHONE: 650/255-1489
                                                                                                                                                                                                                                                                   326 HFIGNCVSSFTAFVKRERDLQGRPSSFFGMDRPPKLRDEF 365
                                                                                                                                                                                                                                                                                                       126 HFIGNCVSSFTAFVKRERDLQGXPSSFFGMDRPPKLRDEF 165
                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-774-954-8
; Sequence 8, Application US/09774954
; Sequence 8, Application No. US20040241645A1
; GENERAL INFORMATION:
; TITLE OF INVENTION: O-PROSPLICANT: TITLE OF INVENTION: O-PROSPLICANT: CORRESPONDENCE ADDRESS:
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STRE: Callifornia
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                                276 DEYFGDIPGGFDLNOMGSRKKWLEKFPSEEYPVLAFSSAPAPFPSKGKVWSIQKYLRWSS 335
                                                                                                                                                                                         254 PLIMIMCLPDLKEIQRAVKLWVRSLDAQSVYVAIDSESYVPELQQLFKGKVKVVSLKPEV 313
                                                                                                                                                                                                                                -----LEO----IEAHROEPDD 420
139 SELFTGI -- SFSASY--- REQWSQRFSPKEHPVLALPGAPAQFPVLEEHRPLQKYMVWSD 193
                                                                                           194 EMVKTGEAQIHAHLVRPYVGIHLRIGSDWKNACAMLKDGTAGSHFMASPQCVGYSRSTAA 253
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                                                                                                                                                                                                                                                                                    314 AQVDLYILGQADHFIGNCVSSFTAFVKRERDLQG---RPSSFFGM 355
                                                                                                                                                                                                                                                                                                               ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                Second 9, Application US/09774954
Publication No. US20040241645A1
GENERAL INFORMATION:
APPLICANT: Yang Wang, Michael W. Spellman
TITLE OF INVENTION: O-Fucosyltransferase
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
STREET: 1 DNA Way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/978,741 FILING DATE: 26-NOV-1997 APPLICATION NUMBER: 08/792,498 FILING DATE: 31-JAN-1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/774, 954
FILING DATE: 30-Jan-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P1041P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                        395 -LTKEIČSPSKQQİ------
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INFORMATION FOR SEQ ID NO: 9:
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US-09-774-954-9
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JONES, Karen Anne; WARREN, Bridget;
JONES, Karen Anne; WARREN, Bridget;
JUNGAVELU, KARLAN; HOUGHELL, Cynthia;
JUNESY, Helen E.;HAFALIA, April J.A.; Huijun Z. Ring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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Best Local Similarity 91.5%; Pred. No. 1.8e-22;
Matches 54; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: 1BM PC compatible
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winbatin (Genentech)
CURRENT APPLICATION DATR:
APPLICATION NUMBER: US/09/774,954
FILING DATE: 30-Jan-2001
CLASSIFICATION ATA:
APPLICATION NUMBER: US/08/978,741
FILING DATE: 26-NOV-1997
ATTORNEY/AGENT INFORMATION:
NAME: SYODOGA, CTaig G.
REFERRALION NUMBER: 39,044
REFERRANE/DOCKET NUMBER: 91041P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SWARNAKAR, Anita; YUB, Henry;
ELLIOTT, Vicki S.; BURFORD, Nell;
DING, Li; TANG, Y. Tom;
ELEB, Soo Yeun; AZIMZAL, Yalda;
CHAWLA, Narinder K.;GIETZEN, Kimberly J.;
GRIEFIN, Jennifer A.; LAL, Preeti G.;
YANG, Junming; BOROWSKY, Mark L.;
RICHARDSON, Thomas W.; YUB, Hulbin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: JACKSON, Jennifer L.; BAUGHN, Mariah R.;
Sequence 3, Application US/09774954
Publication No. US20040241645A1
GENERAL INFORMATION:
TITLE OF INVENTION: O-Eucosyltransferase
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                        ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 61 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: Amino Acid
                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-774-954-3
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APPLICANT:
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APPLICANT:
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ORGANISM: DROSOPHILA
US-11-097-143-36192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               131 ------LQSY 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 152 REGWSGRFSPKEHPVLALPGAPAGFPVLEEHRPLGKYMV----WSDEMVKTGEAQIHAH 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            144 AEGWKE--GTWEEKV-------10ERPCIDQLLYFQEDWMKWKVKLGSA---- 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                207 LVRPYVGIHLRIGSDWKNACAMLKDGTAGSHFWASPQCVGYSRSTAAPLTWTMCLPDLKB 266
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8.3%; Score 164.5; DB 16; Length 328;
Best Local Similarity 21.7%; Pred. No. 6.7e-08;
Matches 85; Conservative 41; Mismatches 115; Indels 151;
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183 LGGPYLGVHLR------RKDFIWGHR------
TITLE OF INVENTION: NUCLEIC ACID ASSOCIATED PROTEINS
FILE REPERROCE: PF-0917 USN
CURRENT APPLICATION NUMBER: US/10/471,450
CURRENT APPLICATION NUMBER: US/10/471,450
PRIOR APPLICATION NUMBER: PCT/USO2/07869
PRIOR PELING DATE: 2002-03-14
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-04-19
PRIOR FILING DATE: 2001-04-19
PRIOR PLILING DATE: 2001-04-19
PRIOR PLILING DATE: 2001-04-19
PRIOR PLILING DATE: 2001-05-04
PRIOR FILING DATE: 2001-05-04
PRIOR PLILING DATE: 2001-05-04
PRIOR PLILING DATE: 2001-05-10
PRIOR PLILING DATE: 2001-05-10
PRIOR PLILING DATE: 2001-05-11
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OTHER INFORMATION: Incyte ID No: 7503717CD1
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Publication No. US20050208558A1
GENERAL INPORMATION:
APPLICANT: Venter, J. Craig
APPLICANT: et al.
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ORGANISM: Homo sapiens
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US-11-097-143-36192
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TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
TITLE OF INVENTION: DAGSOPHILA GENES.
FILE REPERRACE: CLOOD/28
CURRENT APPLICATION NUMBER: US/11/097,143
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: 60/15/,832
PRIOR APPLICATION NUMBER: 60/16/,191
PRIOR APPLICATION NUMBER: 60/16/,191
PRIOR PILING DATE: 1999-10-05
PRIOR PILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: 60/16/,769
PRIOR PILING DATE: 1999-11-28
PRIOR APPLICATION NUMBER: 60/175,693
PRIOR PILING DATE: 2000-01-12
PRIOR APPLICATION NUMBER: 60/175,693
PRIOR PILING DATE: 2000-01-12
PRIOR PILING DATE: 2000-01-12
PRIOR FILING DATE: 2000-01-12
PRIOR FILING DATE: 2000-03-33
NUMBER OF SEQ ID NOS: 43008
SOFTWARE FRASEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              191 FRDKFERVTDK---PCSEGSLSGGPLLQQAELRVGR---FHCVRFQGSAGLLEKLLREAI 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----GSHFMASPQCVGYSR 249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 AGYLLYCPCMGR-FGNQADHFLGSLAFAKLINR-----TLAVPPWIEYQH-HKPPFTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 LHVSYQKYFKLEPLQAYHRVISLEDFM--EKLAPTHWPPEKRVAYCFEV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    309 LKPE------VAQVDLYILGOADHFIGNCVSSFTAFVKRERDLQG 347
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Sequence 8, Application US/10471450
Sequence 8, Application US/10471450
Sequence 10. US/2040152877A1
GENERAL INFORMATION:
APPLICANT: GACKSON, Jannifer L.; BAUGHN, Mariah R.;
APPLICANT: SWARNKAR, Anita; YUE, Henry;
APPLICANT: ELLIOTT, Vicki S.; BURFORD, Neil;
APPLICANT: BILIOTT, Vicki S.; BURFORD, Neil;
APPLICANT: LEE, Soo Yeun; AZIMZAI, Yalda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               212 VGIHLR---IGSDWKNACAMLKDGTA-----
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Indels
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317 DLYILGQADHFIGNCVSSFTAFVKRERDLQG 347
                                                                              371 DOWICAHARFFIGTSVSTFSFRIHEEREILG 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ) NAME/KEY: misc feature
; OTHER INFORMATĪON: Incyte Clone No: 1647884
US-10-820-474A-102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 145078, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                       Sequence 102, Application US/10820474A Publication No. US20050155089A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24 MPAGSWDPAGYLLYCPCMGK 43
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PATTERSON, CHANDRA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TANG, Y. TOM
GORGONE, GINA A.
CORLEY, NEIL C.
GUEGLER, KARL J.
BAUGHN, MARIAH R.
AKERBLOM, INGRID E
AU-YOUNG, JANICE
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: LAL, PREETI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS:
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APPLICANT:
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | :: ::: |:||||: | ::| ::| 313 VRKIRSLMKTHRLDKVFVATDAVR--KEYEELKKTLPEMVRFEPTWEELELYKDGGVAII 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92 THWPPEKRVAYCFEVAAQRSPDKKTCPMKEGN----PFGPFWDQFHVSFNKSELFTG-- 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           145 ------REQWSQRFS 160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      161 PKEHPVLALPGAPAQFPVLEEHR-------PLOKYMWWSDEMVKTGEAQIHAHL 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ------MVFARHLREVGDEFRSRHLNSTDDADRIPFQE--DWMKWKVKLGSA-----L 284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 7.2%; Score 142; DB 16; Length 429; Best Local Similarity 22.0%; Pred. No. 2.1e-05; Matches 99; Conservative 46; Mismatches 138; Indels 168; Gaps
                                         APPLICANT: GRIFFIN, Jennifer A.; LAL, Preeti G.;
APPLICANT: YANG, Junming; BOROWSKY, Mark L.;
APPLICANT: RICHARDSON, Thomas W.; YUE, Huibin;
APPLICANT: BECHA, Shanya; FORSYTHE, Ian J.;
APPLICANT: JONES, Karen Anne; WARREN, Bridget;
APPLICANT: THANGAVELU, Kavitha; HONCHELL, Cynhia;
APPLICANT: JOLLEY, Helen E.; HAFALIA, April J.A.; Huijun Z. Ring
TITLE OF INVENTION: NUCLEIC ACID ASSOCIATED PROTEINS
         CHAWLA, Narinder K.; GIETZEN, Kimberly J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      285 GGPYLGVHLR-------RKDFIWGHR-----
                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: PF-0917 USAN
CURRENT APPLICATION NUMBER: US/10/471,450
FRIOR PLLING DATE: 2003-09-10
PRIOR PLLING DATE: 2003-09-14
PRIOR FLLING DATE: 2002-03-14
PRIOR FLLING DATE: 2002-03-14
PRIOR FLLING DATE: 2001-03-16
PRIOR FLLING DATE: 2001-03-16
PRIOR FLLING DATE: 2001-04-19
PRIOR PLLING DATE: 2001-04-19
PRIOR PLLING DATE: 2001-04-19
PRIOR PLLING DATE: 2001-04-19
PRIOR PLLING DATE: 2001-05-04
PRIOR PLLING DATE: 2001-05-04
PRIOR PLLING DATE: 2001-05-04
PRIOR PLLING DATE: 2001-05-04
PRIOR PLLING DATE: 2001-05-10
PRIOR PLLING DATE: 2001-05-10
PRIOR PLLING DATE: 2001-05-11
PRIOR PLLING DATE: 2001-11-16
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PERL PROGRAM
SEQ ID NO 8

LENGTH 1429
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, OTHER INFORMATION: Incyte ID No: 7493913CD1
US-10-471-450-8
                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: PF-0917 USN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       240
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APPLICANT: LA Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: La Rovalic David K
APPLICANT: Stovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERBNCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 145078
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APPLICANT: HILLMAN, JUNIFER L.
APPLICANT: HILLMAN, JUNIFER L.
APPLICANT: BANDWAN, OLGA
TITLE OF INVENTION: SIGNAL PEPTIDE-CONTAINING MOLECULES
FILE REFERENCE: 039386-1568
CURRENT APPLICATION NUMBER: 08/10/820,474A
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: 09/720,533
PRIOR FILING DATE: 2001-03-20
PRIOR FILING DATE: 2001-03-20
PRIOR FILING DATE: 1999-06-25
PRIOR FILING DATE: 1999-06-26
PRIOR APPLICATION NUMBER: 60/094,983
PRIOR APPLICATION NUMBER: 60/094,983
PRIOR APPLICATION NUMBER: 60/094,983
PRIOR APPLICATION NUMBER: 60/102,686
PRIOR APPLICATION NUMBER: 60/102,686
PRIOR APPLICATION NUMBER: 60/102,686
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Sequence 162121, Application US/10437963
Sequence 162121, Application No. US200401233431
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: ADOU, Yihua
APPLICANT: ADOU, Yihua
APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Buckharov, Andrey A.
APPLICANT: Li, Ping
ITILE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
ITILE OF INVENTION: Blants and Uses Thereof for Plant Improvement
ITILE OF INVENTION: Diants and Uses Thereof for Plant Improvement
FILE REFREENCE: 30-21(53211)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 16221
LENGTH: 441
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Best Local Similarity 19.9%; Pred. No. 0.1;
Matches 77; Conservative 63; Mismatches 147; Indels 99; Gaps 17;
                                                                                                                                                                                                     23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       428 -----DAPIIYLSTDAAESETGILQSLVVLNGRPVPLVIRPARNSAEKWDALLYRHNM 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  302 IMSKPEAVWDE--DTRKPKKKTVQ----DVLGKF-----SFDDDVMAIGDVFYAEVERE 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       350 WVMQ------DGGPIAHKCKTLIEPNRLI-------LLTAQRFIQTFLGRNF 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              389 IALHFR-----RHGFLKFCNAKKPSCFYPIPQAAD------CI--LRVVEMA- 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             272 KLWVRSLDAQSVYVATD-SESYVPELQQL--FKGKVKVVSLKPE------312
                                                                                                                                                                                                                                                                                                                                                                      248 INKCLGKKVVVSFDVFSNLKKGHLHIDKFLCYFS-QPQPCY----LDDBRLKKLGALGL 301
                                                                                                                                                                                                                                                                                                                                                                                                                                   95 PPEKRVAYCFEVAAQRSPDKKTCPMKEGNPFGPFWDOFHVSFNKSELFTGISFSASYREQ 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       155 WSQRFSPKEHPVLALPGAPAQF---PVLEEHRPLQKYWVWSDEMVKTGEAQIHAHLVRPY 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   212 VGIHLRIGSDWKNACAMLKDGTAGSHFWASPQCVGYSRSTAAPLTWTWCLPDLKEIQRAV 271
                                                                                                                                                                                                                                                                                       190 WNPKDGKFLLAICVS--GOMSNHLICLEKHIFFAALLNRVLVIPSSKVDYQYDRVVDIDH 247
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                                                                                                                                                                                                                                               6 WDPA-GYLLYCPCMGRFGNQADHFL---GSLAFAKLLNRTLAVP-PWIEYQHHK-----
                                                                                                                                                                                                                                                                                                                                         55 ------PPFTNL---HVSYQK---YFKLEPLQAYHRVISLED-FMEKLAPTHW
                                                                                                                                                      Query Match 5.9%; Score 117; DB 15; Length 543;
Best Local Similarity 22.0%; Pred. No. 0.012;
Matches 89; Conservative 50; Mismatches 137; Indels 128; Gaps
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                                                                               ; OTHER INFORMATION: Clone ID: PAT_MRT3847_102023C.1.pep
US-10-424-599-145078
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US-10-437-963-162121
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ORGANISM: Oryza sativa
                       TYPE: PRT
ORGANISM: Glycine max
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US-10-437-963-162121
LENGTH: 543
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Thu Oct 27 11:17:25 2005

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Add56824 Novel can
Aad07629 Human sec
Abl13946 Drosophil
Abl13894 Drosophil
                                                                                                                                                                      Ada21151 Human sec
Abs7886 Human cDN
Ads96503 Drosophil
Ab125967 Drosophil
Ab225966 Drosophil
Ada21150 Human sec
Abs73868 Human sig
Ab125964 Drosophil
Ada21178 Human sec
Ada21264 Brosophil
Ada21178 Human oRF
Ada21269 Human ORF
AG52262 Arabidops
Adg7980 Human can
Adg97980 Human CON
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Aaf21609 Neisseria
Aan91052 Phage DNA
Aag05241 Sequence
Adb57903 Toxicity-
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Abr18548 Aspergill
Aar73291 Human imm
Abr17954 Aspergill
Aac94555 Arabidops
Aaa81497 N. mening
                                                                                 Aak79915 Human imm
Aa103342 Human rep
Ach32225 Human end
Ab113952 Drosophil
Ach35332 Human end
Aaf23894 Human sec
Ada21149 Human sec
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O-fucose; inhibitor; sensory neuron; retinal neuron; human; heart; ss.
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/note= "this actively expressed O-fucosyltransferase
sequence is claimed for in claim 9"
1...1098
Aak52494 Human
Aav65634 First
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/*tag
/product= "human heart O-fucosyltransferase"
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AAD07629
ABL13946
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-MODEL=frame+p2n.model -DEF=xlh
-MODEL=frame+p2n.model -DEF=xlh
-Q=/Con2 1/USP3TO spool h/USO9774954/runat 25102005_105431_6380/app_query.fasta_1.917
-Q=/Con2 1/USP3TO spool h/USO9774954/runat_25102005_105431_6380/app_query.fasta_1.917
-DEN Geneege -OFMT=fastap -SUFFTX=rng -MINMATCH=0.1 -LOOFCL=0 -LOOFEXT=0
-UNIT$\overline{S}=bits -START=1 -BND=-1 -MATRIX=blosum62 -TRANS=human40 cdi -LIST=45
-UNIT$\overline{S}=bits -START=1 -BND=-1 -MATRIX=blosum62 -TRANS=human40 cdi -LIST=45
-UNIT$\overline{S}=bits -START=1 -BND=-1 -MAXEN=200000000
-USFR=USO9774954 @CGN 1 1 703 @runat 25102005 105431 6380 -NOPU=6 -ICPU=3
-NO WMAP -LARGEQUERY -NEG SCORES=0 -MAIT -DSPBILOK=100 -LONGLOG
-DSV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPPEXT=0.5 -FGAPPD=6
-FGAPEXT=7 -YGAPPCP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Adf81754 Leukaemia
Aav65633 Plasmid c
Aak51510 Human pol
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                                                                                                                                                                                                                                                                                          8780412
                GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                               nucleic search, using frame plus p2n model
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Maximum Match 100%
Listing first 45 summaries
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Match Length DB
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Database

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Searched:

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481 CCAAAGGAACATCCGGTGCTTGCCCTGCCAGGAGCCCCAGCCCAGTTCCCCGGTCCTAGAA
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                                                                                                                                                  This DNA encodes a human heart O-fucosyltransferase that can glycosylate an epidermal growth factor (ESP) domain of a polygeptide with an activated O-fucose residue. Inhibitors of O-fucosyltransferase, activated O-fucose residue. Inhibitors of O-fucosyltransferase, mutants with increased affinity for the EFG domains, are used in diagnosis and treatment of conditions associated with overexpression of C-fucosyltransferase, to promete survival of sensory (retinal) neurons. Probes based on EMF domain polypeptide are used to detect gene amplification and expression. The expression can also be determined at the protein level using antibodies specific for O-fucosyltransferase
                                                                                                                                                                                                                                                                                                                                              PheGlyAsnGlnAlaAspHisPheLeuGlySerLeuAlaPheAlaLysLeuLeuAsnArg 40
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                                                                                               Human O-fucosyl:transferase able to glycosylate epidermal growth factor domains - useful for diagnosis and treatment of diseases involving overexpression of the enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                   HisValSerTyrGlnLysTyrPheLysLeuGluProLeuGlnAlaTyrHisArgValIle
                                                                                                                                                                                                                                         Sequence 1514 BP; 320 A; 435 C; 411 G; 348 T; 0 U; 0 Other;
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Matches:
Conservative:
Mismatches:
Indels:
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                                       (GETH ) GENENTECH INC.
                                                        Wang Y, Spellman MW;
                                                                        WPI; 1998-437477/37.
P-PSDB; AAW80571.
                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
Query Match:
DB:
              31-JAN-1997;
26-NOV-1997;
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                      GlnSerValTyrValAlaThrAspSerGluSerTyrValProGluLeuGlnGlnLeuPhe
                                                                                                                                                                                                                                                                                                                                           SerProGlnCysValGlyTyrSerArgSerThrAlaAlaProLeuThrMetThrMetCys
                                                                                AspTrpLysAsnAlaCysAlaMetLeuLysAspGlyThrAlaGlySerHisPheMetAla
                                                                 AlaGlnIleHisAlaHisLeuValArgProTyrValGlyIleHisLeuArgIleGlySer
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Leukaemia-related DNA sequence #2310
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30-APR-2002; 2002EP-00009758
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                                                                                                                                              The invention relates to human tumour-associated antigenic target (TAT) polypeptides, and their related nucleic acids. The TAT polypeptides are overexpressed in cancer tissues compared to normal tissues, and may thus serve as effective targets for the diagnosis and treatment of cancer in mammals. The invention also relates to nucleic acid and polypeptide commands. The invention also relates to nucleic acids and polypeptide and polypeptide and polypeptide and polypeptide and expected and methods and compositions for the treatment or TAT polypeptide; and methods and compositions for the treatment or TAT polypeptide, mucleic acids, antibodies, antagonists, binding molecules and compositions are useful for diagnosing or treating a cell proliferative disorder associated with increased TAT expression, particularly cancers such as breast cancer, colorectal cancer, lung cancer, carvical cancer, liver cancer, bladder cancer, pancreatic cancer, cervical cancer, cancer acids may further be used as hybridisation probes, in chromosome and gene mapping, in chromosome identification and in gene therapy. The present sequence
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                                           New tumor-associated antigenic target polypeptides and nucleic acids, useful in preparing a medicament for treating or detecting a proliferative disorder, e.g. breast, lung, colorectal, ovarian or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5218 BP; 1255 A; 1274 C; 1334 G; 1355 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to a method (M1) for determining the subtype of leukaemia cells and whether a patient sample contains leukaemia cells. The method comprises determining the expression profile of a group of markers in a patient sample. The method is useful for determining the presence of leukaemia cells, its types or subtypes, and for the preparation of a medicament for treating leukaemia.
                                                                  Determining the subtype of leukemia cells and whether a patient sample contains leukemia cells or other cells, useful for treating leukemia, comprises determining the expression profile of a group of markers in a patient sample.
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O-fucose, inhibitor; sensory neuron; retinal neuron; human; heart; ss.
                         Plasmid construct for expression of human O-fucosyltransferase.
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                                                                                                   This represents the nucleotide sequence of the plasmid construct used for the expression of human heart O-fucosyltransferase. The human O-fucosyltransferase can glycosylate an epidermal growth factor (BGF) domain of a polypeptide with an activated O-fucose residue. Inhibitors of O-fucosyltransferase, e.g. mutants with increased affinity for the EFG domains, are used in diagnosis and treatment of conditions associated with overexpression of O-fucosyltransferase, to promote auravival of sensory (retinal) neurons. Probes based on EGF domain polypeptide are used to detect gene amplification and expression. The expression can also be determined at the protein level using antibodies specific for O-
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                                     Human O-fucosyl:transferase able to glycosylate epidermal growth factor domains - useful for diagnosis and treatment of diseases involving
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       WPI; 1998-437477/37
P-PSDB; AAW80573.
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  AlaglnileHisAlaHisLeuValArgProTyrValGlyIleHisLeuArgileGlySer
                                 GCCCAGATTCATGCCCACCTTGTCCGGCCCTATGTGGGCCATTCATCTGCGCATTG
                                                                                             ASpTrpLysAsnAlaCysAlaMetLeuLysAspGlyThrAlaGlySerHisPheMetAla
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27-AFR-2000; 2000US-00566875.
20-JUN-2000; 2000US-00598075.
19-JUJ-2000; 2000US-00654936.
15-SEP-2000; 2000US-00654936.
20-CT-2000; 2000US-0063325.
30-NOV-2000; 2000US-00728422.
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(HYSE-) HYSEQ INC
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                                                                             Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy.
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                                                                                                                                    Claim 1; Page 638-642; 6221pp; English.
Yang Y, Wejhrman T,
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P-PSDB; AAM78377.
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2000US-00594916.
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2000US-0059315.
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WPI; 1998-437477/37.
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                                                                               Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy.
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 Y;
Wang ?
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 Xu C, Cao
Chen R,
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Asundi V, Zhou P,
J, Zhang J, Ren
Goodrich R;
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                    Claim 1; Page 4424-4425; 6221pp; English
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 Drmanac RT, A
Wang D, Wang J
Wejhrman T, G
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1855.50
96.70%
95.60%
                                             WPI; 2001-476283/51.
P-PSDB; AAM79361.
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Best Local Similarity:
 Tang YT, Liu C,
Ma Y, Zhao QA, V
Xue AJ, Yang Y,
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                                                                                                                                                                                                                                                                                               880 CCGCAGTGTGGGCTACAGCCGCACAGCACAGCCCCCCTCACGATGACTATGTGCCTG
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                                                                                                                                                                                                   ProGlnCysValGlyTyrSerArgSerThrAlaAlaProLeuThrMetCysLeu
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                          TrpLysAsnAlaCysAlaMetLeuLysAspGlyThrAlaGlySerHisPheMetAlaSer
  HisArgProLeuGlnLysTyrMetValTrpSerAspGluMetValLysThrGlyGluAla
                                                                                     GlnIleHisAlaHisLeuValArgProTyrValGlyIleHisLeuArgIleGlySerAsp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          First EcoR1 nucleotide fragment of human KIAA0180
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This represents a first EcoR1 nucleotide fragment of human KIAA0180. This 5009 basepairs partial CDNA encodes for a protein of unknown function from wpeblast cel line KG-1. The invention provides a human heart O-fucosyltransferase that can glycosylate an epidermal growth factor (EGF) domain of a polypeptide with an activated O-fucose residue. Inhibitors of O-fucosyltransferase, e.g. mutants with increased affinity for the EFG domains, are used in diagnosis and treatment of conditions associated with overexpression of O-fucosyltransferase, to promote survival of sensory (retinal) neurons. Probes based on EGF domain polypeptide are used to detect gene amplification and expression. The expression can also be determined at the protein level using antibodies specific for O-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CyspheGluValAlaAlaGlnArgSerProAspLysLysThrCysProMetLysGluGly 122
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                                                                                                                                                                                                                                                                                                                                                                                                             43 AlaValProProTrpIleGluTyrGlnHisHisHisLysProProPheThrAsnLeuHisVal
                                                                                                                                                                                                                                                                                                                                                               23 AsnGlnAlaAspHisPheLeuGlySerLeuAlaPheAlaLysLeuLeuAsnArgThrLeu
domains - useful for diagnosis and treatment of diseases involving overexpression of the enzyme.
                                                                                                                                                                                                                Sequence 5009 BP; 1235 A; 1195 C; 1268 G; 1311 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
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                                   Example 1; Fig 11; 90pp; English
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1844.00
100.00%
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93.18%
                                                                                                                                                                                             fucosyltransferase
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                                                                                                                                                 323 GlnAlaAspHisPheIleGlyAsnCysValSerSerPheThrAlaPheValLysArgGlu
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                                                                                                                                                                                                                                                                   962 CGGGACCTCCAGGGGGGGCCGTCTTTTTTTCGGCATGGACAGGCCCCCTAAGCTGCGG
AspleuLysGlulleGlnArgAlaValLysLeuTrpValArgSerLeuAspAlaGlnSer
                                                                 GACCTGAAGGAGATCCAGAGGGCTGTGAAGCTCTGGGTGAGGTCGCTGGATGCCCAGTCG
                                                                                                   ValTyrValAlaThrAspSerGluSerTyrValProGluLeuGlnGlnLeuPheLysGly
                                                                                                               343 ArgAspleuGlnGlyArgProSerSerPhePheGlyMetAspArgProProLysLeuArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             developmental biology; cell signalling; insecticide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 36323; 21pp + Sequence Listing; English.
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11-JUL-2000; 2000US-00614150.
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pharmaceutical; gene; ss
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1022 GACGAGTTC 1030
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                                                                                                                                                                                                                                                                           27 HisPheLeuGlySerLeuAlaPheAlaLysLeuLeuAsnArgThrLeuAlaValProPro
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TCTAAGGATTTCAFCCGAGAGCAGTTGCCTCGGGGTGCCTTTTTGGGCATTCATCTGCGC
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ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                      7 AspProAlaGlyTyrLeuLeuTyrCysProCysMetGlyArgPheGlyAsnGlnAlaAsp
                                                                                                                                                                                                                                                82 GATCCCAATGGCTACCTCACCTACTGTCGTGTATGGGACGCTTTGGCAACCAGGCCGAC
                                                                                                                                                                                                                                                                                                                                                                                      TyrPheLysLeuGluProLeuGlnAlaTyrHisArgValIleSerLeuGluAspPheMet
                                                       Seguence 1209 BP; 302 A; 313 C; 307 G; 287 T; 0 U; 0 Other;
                                                                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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831.00
61.23%
44.65%
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This invention is related to a novel isolated canine nucleic acid sequences and the construction of canine microarrays containing a significant portion of the canine genome. The isolated canine nucleic significant portion of the canine genome. The isolated canine nucleic coid sequences of the invention may be useful for drug screening and toxicity assays. The invention is therefore useful for assessing the impact, including toxicity, of a compound, pharmaceutical agent or environmental pollutant on a call or living organism. The methods are useful for detecting genes that are up- or down-regulated in canines in a seaful for detect a callular response in a sample individually or as part of a gene expression profile. It is also useful as a target for agents that modulate gene expression or activity. The database is useful for producing electronic Northerns that allow the user to determine the cell type or tissue in which a given gene is expressed and to allow the abundance or expression level of a given gene in a
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Or
                                                                                       CACATGATTGGTGAACTAAACACGGCCCTTAGTCGCATGGGCATCAGTGTGCACAAGCTG
                                                                                                                                                    1024 CCGGAGGATGATCCTTACCTGGACTTGGCCATTCTCGGACAGTCGAACCACTTTATCGGC
                                                                                                                               310 LysProGluValAlaGlnValAspLeuTyrIleLeuGlyGlnAlaAspHisPheIleGly
                                                                                                                                                                                                         AsnCysValSerSerPheThrAlaPheValLy8ArgGluArgAspLeuGlnGlyArgPro
                                                      291 SerTyrValProGluLeuGln---GlnLeuPheLysGlyLysValLysValValSerLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 canine microarray; drug screening; toxicity assay;
environmental pollutent; cellular response; gene expression profile;
toxic response; liver necrosis; fatty liver disease;
protein adduct formation; hepatitis; dog; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated nucleic acid molecule, useful for drug screening and toxicity assays or for assessing the impact, including toxicity, of compound, pharmaceutical agent or environmental pollutant on a cell
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1144 TCGTACTTCTGGGGATTC-----CCCAAGGAAAAGGAT 1176
                                                                                                                                                                                                                                                                                   350 SerSerPhePheGlyMetAspArgProProLysLeuArgAsp 363
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living organism.
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particular tissue or cell. The methods are useful for determining the similarity of a toxic response to one or more individual compounds. The methods are useful for predicting at least one toxic response or the likelihood that a compound or teet agent will induce various specific pathologies such as those of the liver (liver necrosis, fatty liver disease, protein adduct formation or hepatitis), those of the kidney, theart, brain or testes, or other pathologies associated with at least of the toxins. The methods are also useful for predicting or elucidaring the potential callular pathways influenced, induced or modulated by the compound or test agent due to the similarity of the expression profile compound or the profile induced by a known toxin. The present sequence is that of a canine phy sequence which was claimed for use during the production of a canine microarray of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                182 CCCATGAAGGAAAGGAAATCCCTTTGGCCCCATTTTGGGATCAGTTTCATGTGAGTTTCAAC
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                                                                                                                                                                                                                                                                                                                                                78 ArgVallleSerLeuGluAspPheMetGluLysLeuAlaProThrHisTrpProGlu
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                                                                                                                                                                              Sequence 610 BP; 155 A; 171 C; 149 G; 129 T; 0 U; 6 Other;
                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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AMD07571-AAD07645 represent cDNAR corresponding to 25 human secreted protein genes, and AAE03052-AAE0316 represent the proteins they encode. AAE03127-AAE03150 represent human secreted protein fragments. The genes and their corresponding secreted proteins fragments. The genes can their corresponding secreted proteins are useful for preventing, retaining to amelicating medical conditions, e.g., by protein or gene therapy. Pathological conditions can be diagnosed by determining the presence of mutations in the new genes. Specific uses are described for each of the matter in the new genes. Specific uses are described for each of the mitted developing products for the diagnosis or treatment of an include developing products for the diagnosis or treatment of an include developing products for the diagnosis or treatment of abnormalities, haematopoietic disorders, diseases of the immune system, abnormalities, haematopoietic disorders, diseases of the immune system, and include disorders, schizophrenia, asthma, skin disorders disorders disorders, schizophrenia, asthma, skin disorders disorders, angiogenic disorders, kidney disorders, and disorders and also be used to and wound healing and event by and appropriate disorders and also be used to and wound and disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    occurring L-amino
focetal abnormality; developmental abnormality; haematopoietic disorder; immune system disorder; ALDS; autoimmune disease; rhematoid arthritis; inflammation; allaery; neutrological disorder; Alzheimer's disease; Parkinson's disease; cognitive disorder; schizophrenia; asthma; stim disorder; psoriaais; sepsis; diabetes; artherosclerosis; cardiovascular disorder; anglogenic disorder; kidney disorder; gastrointestinal disorder; anglogenic disorder; kidney disorder; ene endocrine disorder; infection; wound healing; vulnerary; cell culture; chemotaxis; food additive; binding partner identification; chromosome 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acids encoding 25 human secreted polypeptides, useful for preventing, disposing and/or treating e.g. Gaucher's disease, Alzheimer's disease, Scimitar syndrome, Creutzfeldt-Jacob disease, diabetes mellitus and multiple sclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                 forduct = "Human secreted protein precurs forance | Post-4. 6, as.Xaa) | fransl except= (pos.10. .12, as.Xaa) | fransl except= (pos.10. .12, as.Xaa) | fransl except= (pos.13. .15, as.Xaa) | fransl except= (pos.42. .444, as.Xaa) | fransl except= as.Xaa | fransl except= as.Xaa | fransl except= (pos.42. .444, as.Xaa) | fransl except= (pos.44, as.Xaa) | fransl except= as.Xaa equals any of the naturally o acids; CDS does not include start codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Mature human secreted protein"
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                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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21-JUL-2000; 2000US-0219666P.
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P-PSDB; AAE03110.
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primary tissues, to regenerate tissues, to identify their cognate ligands or binding partners, and in chemctaxis, and can be used as a food additive or preservative to modify storage properties. Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The present sequence represents a human secreted protein-encoding CDNA of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             345
                                                                                                                                                                                                                                                                                                                                                                                       246 GlyTyrSerArgSerThrAlaAlaProLeuThrMetThrMetCysLeuProAspLeuLys 265
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                                                                                                                                                                                                                                                                                        206 HisLeuValArgProTyrValGlyIleHisLeuArgIleGlySerAspTrpLysAsnAla
                                                                                                                                                                                                                                                                                                    16 CACTITICCCGAACCIACCCGGGCAITCAICTGCGCAITGGCICTGACIGGAAGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                       266 GluileGlnArgAlaValLysLeuTrpValArgSerLeuAspAlaGlnSerValTyrVal
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Matches:
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                                                                                                                                       Sequence 915 BP; 209 A; 253 C; 247 G; 202 T;
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                                                                                                                                                                                                                                                                                         The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                           detection reagent for detecting 1000 or more for elucidating cell signaling and cell-cell
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                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 36320; 21pp + Sequence Listing; English.
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11-JUL-2000; 2000US-00614150.
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58.27%
42.49%
40.22%
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genes from Drosophila and
interactions.
                                                                                                               Adams M,
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                                                                                (PEKE ) PE CORP NY
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Best Local Similarity:
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1301 CCAAACTCAGCCGGACAACGAATCAATCAGTTTTCGTGGCGTCAGACTCCAATCACAT 1242
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                                                                                   292 rValProgluLeuGln---GlnLeuPheLysGlyLysValLysValValSerLeuLysPr 311
                                                                                                                                                                                                                                                                                                                                                                  SValSerSerPheThrAlaPheValLysArgGluArgAspLeuGlnGlyArgProSerSe 351
               219 YSerAspTrpLysAsnAlaCysAlaMetLeuLysAspGlyThrAlaGlySerHisPheMe 239
                                                                                                                                                                               239 tAlaSerProGInCysValGlyTyrSerArgSerThrAlaAlaProLeuThrMetThrMe 259
                                                                                                                                                                                                                     259 tCysLeuProAspLeuLysGluileGlnArgAlaValLysLeuTrpValArgSerLeu-- 278
                                                                                                                                                                                                                                                         143 rGlylleSerPheSerAlaSerTyrArgGluGln------TrpSerGlnArgPheSe 160
                                                                                                                        rProLysGluHisprovalLeuAlaLeuProGlyAlaproAlaGlnPheProvalLeuGl
                                                180 uGjuHisArgProLeuGjnLysTyrMetValTrpSerAspGluMetValLysThrGlyGl
                                                                                                           200 ualaGlnIleHisAlaHisLeuValArg---ProTyrValGlyIleHisLeuArgIleGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster expressed polynucleotide SEQ ID NO 36164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                    1061 CTTCTGGGGATTC-----CCCAAGGAAAAGGAT 1034
                                                                                                                                                                                                                                                                                                                                                                                                        rPhePheGlyMetAspArgProProLysLeuArgAsp 363
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ABL13894 standard; cDNA; 3793 BP
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11-JUL-2000; 2000US-00614150.
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rProLysGluHisProValLeuAlaLeuProGlyAlaProAlaGlnPheProValLeuGl 180
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                                                                                                                                  The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher enkaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIG176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA ABD72072). The sequence data for this patent did not form part of bring printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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| GGAGTATCGT-----AGGGGTGAACTGCGATCCCGTCAGGTACCGTTCAACACATATTT
                                                              New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.
                                                                                                                                                                                                                                                                         Sequence 3793 BP; 1020 A; 853 C; 950 G; 970 T; 0 U; 0 Other;
                                                                                                              Claim 1; SEQ ID NO 36164; 21pp + Sequence Listing; English.
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Matches:
Conservative:
Mismatches:
Indels:
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        Li PWD,
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506.50
56.38*
42.39*
25.59*
           Venter JC, Adams M,
                               WPI; 2001-656860/75.
P-PSDB; ABB69791.
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29-SEP-2000; 2000US-023-63-6P.
29-SEP-2000; 2000US-023-63-70P.
02-OCT-2000; 2000US-023-703-P.
02-OCT-2000; 2000US-023-703-P.
03-OCT-2000; 2000US-023-703-P.
03-OCT-2000; 2000US-023-99-1P.
03-OCT-2000; 2000US-023-99-1P.
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03-OCT-2000; 200US-024-10-P.
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03-OCT-2000; 2000US-024-10-P.
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2000US-0232399P.
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220
                           180 uGluHisArgProLeuGlnLysTyrMetValTrpSer-AspGluMetValLysThrGlyG 200
                                                                                                                ------ATAGGGAAGCATCTAAGGATTTCAT 13
 141 TGCAGAATCATATCCCGTACTCGCGTTCACCGGAGCTCCGGCTAGTTTTCCTGTTCAGCT
                                                                                    200 luAlaGlnIleHisAlaHisLeuValArgProTyrValGlyIleHisLeuArgIleGlyS
                                                                                                                                                                                                                                                                                                                                                Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                                                                                                                                                                                                                                                                    Human immune/haematopoietic antigen genomic sequence SEQ ID NO:34727
                                             AAK79915 standard; DNA; 10331 BP
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2000US - 022547P
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2000US-0198123P.
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2000US-0224519P.
2000US-025213P.
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2000US-0225266P.
2000US-0225267P.
2000US-025268P.
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                                                                                                                                                                                                                                                                                            07-NOV-2001 (first entry)
                                                                                                                                              220 erAsp 221
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07 - JUL - 2000;
11 - JUL - 2000;
11 - JUL - 2000;
14 - JUL - 2000;
26 - JUL - 2000;
14 - AUG - 2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-JUN-2000;
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263 AspleutysGluIleGlnArgAlaValLysLeuTrpValArgSerLeuAspAlaGlnSer 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; reproductive system related antigen; reproductive system disorder; cancer; gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                 Human reproductive system related antigen DNA SEQ ID NO: 6032.
                                                                                                                                                                                                                                                                                                    AAL03344 standard; DNA; 10331 BP.
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2000US-0184664P.
2000US-0189814P.
2000US-01991074P.
2000US-0199123P.
2000US-02515P.
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2000US-021886P.
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2000US-021889P.
2000US-021889P.
2000US-022518P.
2000US-022518P.
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2000US-0225267P.
2000US-022547P.
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2000US-0225757P.
2000US-0225759P.
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                                                                                                                                                                                                                   2731 AAGGTATGTGTG 2742
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                                                                                                                                                                                     303 LysyalLysyal 306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAKE4951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have eytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polymuclectides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polymuclectides may be used to produce the secreted (I), by inserting the concleic acids into a host cell and culturing the cell to express the diagnose and treat immune/haematopoietic-derived cells. AAK64703 to AAK87694 represent human immune/haematopoietic derived cells. AAK64703 cancers and cancer metastases of haematopoietic derived cells. AAK64703 represent human immune/haematopoietic antigen genomic sequences from the present invention. AKM54942 to AAK64950 and AAM93169 represent success and in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GlnCysValGlyTyrSerArgSerThrAlaAlaProLeuThrMetThrMetCysLeuPro 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acide encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 34727; 3071pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 10331 BP; 2718 A; 2405 C; 2599 G; 2609 T; 0 U; 0 Other;
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Matches:
Conservative:
Mismatches:
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  17-NOV-2000; 2000US-0249214P.
17-NOV-2000; 2000US-0249215P.
17-NOV-2000; 2000US-024921FP.
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17-NOV-2000; 2000US-024924FP.
17-NOV-2000; 2000US-024929P.
17-NOV-2000; 2000US-0259P.
17-NOV-2000; 2000US-0259P.
17-NOV-2000; 2000US-02519P.
18-DEC-2000; 2000US-02518P.
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Query Match:
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2000US-0236802P

2000US-0237037P

2000US-0237037P

2000US-0237039P

2000US-0239935P

2000US-0241221P

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2000US-0241785P

2000US-0241786P

2000US-0241786P

2000US-0241786P

2000US-0241786P

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2000US-024187P

2000US-0246478P

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2000US-023194P.
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08-NOV-2000;
01-SEP-2000; 201-SEP-2000; 205-SEP-2000; 205-SEP-2000; 206-SEP-2000; 206-SEP-2000; 208-SEP-2000; 208
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21-SEP-2000;
25-SEP-2000;
25-SEP-2000;
26-SEP-2000;
27-SEP-2000;
27-SEP-2000;
29-SEP-2000;
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29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
20-CCT-2000;
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Isolated nucleic acid molecule encoding a reproductive system antigen is used in preventing, treating or ameliorating a medical condition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding a protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 6032; 1297pp + Sequence Listing; English
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Matches:
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17-NOV-2000; 2000US-0249214P.
17-NOV-2000; 2000US-0249215P.
17-NOV-2000; 2000US-0249211P.
17-NOV-2000; 2000US-0249211P.
17-NOV-2000; 2000US-024921BP.
17-NOV-2000; 2000US-024924F.
17-NOV-2000; 2000US-024924F.
17-NOV-2000; 2000US-0249264P.
17-NOV-2000; 2000US-025103P.
05-DEC-2000; 2000US-025109P.
06-DEC-2000; 2000US-0251866P.
08-DEC-2000; 2000US-0251866P.
08-DEC-2000; 2000US-0251866P.
08-DEC-2000; 2000US-0251869P.
08-DEC-2000; 2000US-0251869P.
08-DEC-2000; 2000US-0251869P.
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Query Match:
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11-DEC-2000; 2
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2730

ValTyrvalAlaThrAspSerGluSerTyrValProGluLeuGlnGlnLeuPheLysGly 302

GICTACGITGCTACTGATTCCGAGAGTTATGTGCCTGAGCTCCAACAGCTCTTCAAAGGG

Lysvallysval 306

303

2671

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283

263

요 ò 셤 8

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The invention relates to an isolated polymuclectide comprising any one of 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was determined by the technique of SBH (sequencing by Mybridisation). Also included is a purified polymeptide comprising a sequence corresponding to a reading frame of the novel polymuclectide. The nucleic acid sequences are useful in diagnostics as expressed sequence tags (EST) for identifying expressed genes or for physical mapping of the human genome, in forensics, in assessing biodiversities, or in identifying mutations in forensics, in assessing biodiversities, or in identifying mutations crapponsible for genetic disorders and other traits. The nucleotide responsible for genetic alsorders and other traits. The nucleotide sequences are also useful as hybridisation probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of is useful for generating antisense DNA or RNA. The purified polypeptide is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data for this patent did not form part of the printed specification, but was contained in electronic format directly from USPTO at equation of the command in electronic format directly from USPTO at equation of the SPTO at this process.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New polynuclectide sequences obtained from various cDNA libraries, useful as hybridization probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA.
                                                                                                                                                                                    Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST; genome mapping; biodiversity; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 479 BP; 99 A; 140 C; 143 G; 97 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 19437; 44pp; English.
                                                                                                                                                      Human endothelial cell cDNA #358
                                  ACH32225 standard; cDNA; 479 BP
                                                                                                                                                                                                                                                                                                                                                                             30-JUL-2001; 2001US-00918995.
                                                                                                                                                                                                                                                                                                                                                                                                                  30-JUL-2001; 2001US-00918995.
                                                                                                                 13-OCT-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       (DRWA/) DRWANAC R T.
(LABA/) LABAT I.
(STAC/) STACHE-CRAIN B.
(DICK/) DICKSON M C.
(JONE/) JONES L W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-615964/58.
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Pred. No.:
                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                          17-APR-2003.
                                                                              ACH32225;
RESULT 15
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290 GluSerTyrValProGluLeuGlnGlnLeuPheLysGlyLysValLysValValSerLeu 309

US-09-774-954-2 (1-365) x ACH32225 (1-479)

479 76 0 0 0

Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:

3.9e-32 393.00 100.00% 100.00%

Percent Similarity: Best Local Similarity:

Search completed: October 26, 2005, 09:51:26 Job time : 1056.3 secs 31 음 상 음 ò g à 2731 AAGGTATGTGTG 2742

Thu Oct 27 11:17:25 2005

GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

October 26, 2005, 09:31:14 ; Search time 1559.68 Seconds (without alignments) 1931.299 Million cell updates/sec Run on:

1 MPAGSWDPAGYLLYCPCMGR.....QGRPSSFFGMDRPPKLRDEF 365 US-09-774-954-2 1979 Title: Perfect score: Sequence:

0.5 0.5 0.5 Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext **BLOSUM62** Scoring table:

9772377 segs, 4126317084 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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Database

Published Applications Nh:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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9	g	00	11284	11	19-774-954	equence 5,
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Н	196	٥.	N	56	11-097-143-1816	equence 18.
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13	424	21.4	10331	10	9-764-891-6032	9 60.
14	393	ė.	4	10	19-918-995-1943	equence 194
c 15	392	ď.	3567	56	11-097-143-181	equence 18169,
16	353	7.	477	_	5-09-918-995-2274	Seguence 22744,
17	264	щ.	402		9-783-590-11	11501
18	164.5	•	O	0	5-10-471-450-52	equence 52,
19	164		σ	56	11-097-143-3	equence 361
20	164		3926	56	11-097-143-3619	361
N	142		4	20	10-471-450-3	34,
c 22	120		521	13	39-925-065A-60	0244
~	120		760	24	10-820-474A-23	236
24	117		N	19	10-424-599-223	2236,
c 25	115.5		-	26	11-097-143-361	36187
26	110		S	22	10-764-420-210	2104,
27	109		w	18	10-062-674-187	1876,
28	108		o	22	-10-956-157-414	4145,
29	106.5	٠.	2166	20	10-437-963-59	538
30	9		ß	22	-10-956-157-198	1986,
31	103.5	5.2	096	18	10-309-290	Sequence 119, App
32	8		096	18	-10-309-290-12	121,
33	Н		o	19	-10-425-114-3161	31610
34	103		2122	21	-10-425-115-143	14381
35	5		~	16	-10-128-714-23	2312,
96	102.5		907	16	-10-128-714-131	1312,
37	2		ര	16	-10-128-714-31	312,
0	, –		2790	20	-10-437-963-71	equence 7143
יי נ	102		· c	24	-10-915-740A-44	44, 7
0.4	101		2		S-10-915-740A-	Sequence 1068
. 4	101		1617	C	-10-437-963-114	equence 1143
7	101		2600	4.5	5-10-450-763-10	Sequence 10656, A
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,	3	٠	74399	1 0	-10-287-226-321	e 321,
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ALIGNMENTS

Sequence 16, Application US/09774954

Publication No. US20040241645A1

GENERAL INFORMATION:
TITLE OF INVENTION: O-Fucosyltransferase

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way

CITY: South San Francisco
STREET: California
COUNTRY: USA RESULT 1 US-09-774-954-16

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GlnservalTyrvalAlaThrAspSerGluSerTyrvalProGluLeuGlnGlnLeuPhe 300
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                                                                                                                                                                                                                                   221 ASPTITIVSABINALACYSALAMETLEULVSASPGLYTHIALALAGLYSERHisPheMetAla 3
  COUNTY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy dis

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: MinPatin (Genentech)

CURRENT APPLICATION DMTA:

REPLICATION NUMBER: US/09/714,954

FILING DATE: 30-0an-2001

CLASSIFCATION: CUNKNOWN-

PRIOR APPLICATION NUMBER: US/08/978,741

APPLICATION NUMBER: US/08/978

FILING DATE: 28-NOV-1997

APPLICATION NUMBER: 08/792,498

FILING DATE: 31-JAN-1997
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) S-09-7/4-594-4
) S-09-7/4-594-4
) Publication No. US20040241645A1
| GENERAL INFORMATION:
| TITLE OF INFORMATION:
| TITLE OF INFORMATION: O-PROSECTION O-PROS
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US-09-774-954-4
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COMPUTER READABLE FORM:
MEDIUM TYBE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OVERATING SYSTEM: PC-DOS/MS-DOS
OFFWARE: Winheatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/774,954
FILING DATE: 30-Jan-2001
CLIASSIFICATION NUMBER: US/08/978,741
FILING DATE: 26-NOV-1997
APPLICATION NUMBER: US/08/978,741
FILING DATE: 31-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: SYODOGA CRAIG GREEN SPOORE NUMBER: 39,044
REFERENCE/DOCKET NUMBER: 39,044
REFERENCE/DOCKET NUMBER: 39,044
REFERENCE/DOCKET NUMBER: 39,044
REFERENCE/DOCKET NUMBER: 39,044
TELECHONE: GS0/252-9881
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE THRACTERISTICS:
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE THRACTERISTICS:
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE THRACTERISTICS:
INFORMATION FOR SEQ ID NO: 16:
STRANDEDNESS: SINGIE
TYPE: NUCleic Acid
STRANDEDNESS: SINGIE
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; SEQUENCE DESCRIPTION: SEQ ID NO: 16: US-09-774-954-16
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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                                                                                                                                                                            CTGCCTGACCTGAAGGAGATCCAGAGGGCTGTGAAGCTCTGGGTGAGGTCGCTGGATGCC
                                                                                                                                                                                                                                                                                                                                                     LysGlyLysValValAsValValSerLeuLysBroGluValAlaGlnValAspLeuTyrIle
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                                                                                                                                                                                                                                        GlnSerValTyrValAlaThrAspSerGluSerTyrValProGluLeuGlnGlnLeuPhe
                                                SerProGlnCysValGlyTyrSerArgSerThrAlaAlaProLeuThrMetThrMetCys
                                                                                                                           LeuProAspLeuLysGluIleGlnArgAlaValLysLeuTrpValArgSerLeuAspAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Winpatin (Genentech) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/09774954
Publication No. US20040241645A1
GENERAL INFORMATION:
APPLICANT: Yang Wang, Michael W. Spellman
TITLE OF INVENTION: O-Fucosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR DATE: 30-Jan-2001
CLASSIFICATION NUMBER: US/09/774,954
FILING DATE: 30-Jan-2001
CLASSIFICATION: CUNKNOWN>
PRIOR APPLICATION OFF:
APPLICATION NUMBER: US/08/978,741
RILING DATE: 26-NOV-1997
APPLICATION NUMBER: 08/792,498
FILING DATE: 31-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: SVODOGA, Craig G, REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: 91041P1
TELEPRONE: 650/225-1489
TELEPRONE: 650/225-1489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: Linear SEQUENCE DESCRIPTION: SEQ ID NO: 1: US-09-774-954-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: South San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 1514 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
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STREET: 1 DNA Way
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             496 GAAGGAAACCCTTTGGCCCATTCTGGGATCAGTTTCATGTGAGTTTCAACAAGTCGGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41 ThrLeuAlaValProProTrplleGluTyrGlnHisHisLysProProPheThrAsnLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  436 GCATACTGCTTTGAGGTGGCCAGCCAGCGAAGCCCCAGATAAGAAGACGTGCCCCATGAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     256 ACCTIGGCIGICCCTCCTIGGATIGAGIACCAGCATCACAAGCCTCCTTICACCAACCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PheGlyAsnGlnAlaAspHisPheLeuGlySerLeuAlaPheAlaLysLeuLeuAsnArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Met ProAlaGlySerTrpAspProAlaGlyTyrLeuLeuTyrCysProCysMetGlyArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-774-954-2 (1-365) x US-09-774-954-4 (1-1300)
                                                                                                TELECOMMULCATION INFORMATION:
TELEPHONE: 650/225-1489
TELEPAX: 650/9225-1489
TELEPAX: 650/922-9881
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1300 base pairs
TYPE: NUCLEIC Acid
STRANDEDNESS: Single
TOPOLLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                     NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P1041P1
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ATTORNEY/AGENT INFORMATION:
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& g	361 Leu 1081 CTG	LeuargaspGluPhe 365 crGcGGACGAGTrC 1095	
RESULT US-10 PUBLI REPUBLI	SULT 4 Sequence 168, Applia Sequence 168, Applia Publication No. US2 Seguence 168, Applia Publication No. US2 APPLICANT: Berger APPLICANT: Berger APPLICANT: Schleg APPLICANT: Schleg APPLICANT: Schleg APPLICANT: Schleg APPLICANT: Thibod APPLICANT: Thibod APPLICANT: Thibod APPLICANT: Thibod APPLICANT: MISCONDER TITLE OF INVENTION TITLE OF INVENTION TITLE OF INVENTION FILE REFERENCE: MPI CURRENT FILING DATE: PRIOR FILING DATE: TOWNBER OF SEQ ID N SOGTWARR: FASESEQ SEG ID NO 168 ILBNGTH: 5218 TYPE: DNA CRGANISM: Homo Sa FEATURE: NAME/FEY: CDS LOCATION: (50)	ESGULT 4 Sequence 168 Sequence	, KITS, AND DN, ASSESSMENT, PREVENTION, AND
Alignment Pred. No Score: Percent to Best Loct Query Mat	Alignment Scores: Pred. No.: Score: Score: State Similarity: Best Local Similari Query Match:	: 1.31e-237 Length: 1979.00 Matches: -y: 100.00\$ Conservati arity: 100.00\$ Mismatches 16.00\$ Indels:	5218 365 ive: 0 s: 0
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Matches:
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: PatentIn version 3.2
SEQ ID NO 4752
LENGTH: 5218
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Sequence 4752, Application US/10956157

Sequence 4752, Application US/10956157

Sequence 4752, Application US/0050118625A1

Sequence 4752, Application US/0050118625A1

GENERAL INFORMATION:

APPLICANT: Wyeth

APPLICANT: Wounts, William

TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH

TITLE OF INVENTION: HUMAN OSTBOARTHRITIS AND HUMAN PROTEASES

FILE REFERENCE: 031896-043000 (AM 101081)
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Query Match: 100.00% Indels: 0 DB: 11 Gaps: 0	-2 (1-365) x US-09-774-954-5 (1-11284) MetproAlaGlySerTroAspProAlaGlyTyrLeuLeuTyrCys	4236 AIGCCCGCGGGGCTCCTGGGACCCGGTTACTGCTCTACTGCCCCTGCAIGGGGCGC	21 PheGlyAsnGlnAlaAspHisPheLeuGlySerLeuAlaPheAlaLysLeuLeuAsnArg	60	Db 4356 ACTTGGCTGTCCTTGGATTGAGTACCAGCATCACAGAGCTCCTTTCACCACCTC 4415 Ov 61 HisValSeTVrGlnLvsTvrPheLysLeuGluProLeuGlnAlaTyrHisArgValIle 80	4116 CATGLGTCCTACCAGAAGTACTTCAAGCTGGAGCCCCTCCAGGCTTACCATCGGGTCATC	QY 81 SerLeuGluAspPheMetGluLysLeuAlaProThrHisTrpProProGluLysArgVal 100	101 AlaTyrCysPheGluValAlaAlaGlnArgSerProAspLysLysThrCysProMetLys			Qy 141 LeuPheThrGlyIleSerPheSerAlaSerTyrArgGluGlnTrpSerGlnArgPheSer 160	ч 9	Qy 181 GluHisArgProLeuGlnLysTyrMetValTrpSerAspGluMetValLysThrGly 200	Oy 201 AlaGlnIleHisAlaHisLeuValArgProTyrValGlyIleHisLeuArgIleGlySer 220	Oy 221 ASPITPLYSASNAlaCySAlaMetLeuLySASPGlyThrAlaGlySerHisPheMetAla 240	Oy 241 SerProGlnCysValGlyTyrSerArgSerThrAlaAlaProLeuThrMetThrMetCys 260	Oy 261 LeuProAspLeuLysGlutleGlnArgAlaValLysLeuTrpValArgSerLeuAspAla 280	281	Qy 301 LysGlyLysValValSerLeuLysBroGluValAlaGlnValAspLeuTyrIle 320	Oy 321 LeuGlyGlnAlaAspHisPhelleGlyAsnCysValSerSerPheThrAlaPheVallys 340	
	GlnSerValTyrValAlaThrAspSerGluSerTyrValProGluLeuG	959 CAGICGGILIACGIICCIACIGAIILCCGAGAGIIAIGIGGGCCIGAGGILCCGAGGILTIC 2013 301 LygGlyLygValLygVallyglyglYgilGerLeuLygProGluValAlaGlnValAspLeuTyrile 320	1019 AAAGGGAAGGTGAAGGTGGAGCCTGAAGCTGAGGTGGCCCAGGTCGACTGTACATC 10	Oy 321 LeuGlyGlnAlaAspHisPheIleGlyAsnCysValSerSerPheThrAlaPheValLys 340	341 ArgGluhrgAspLeuGlnGlyArgProSerSerPhebheGlyMetAsp.	7	1199	L 0 +	GENERAL INFORMATION: APPLICANT: Yang Wang, Michael W. Spellman ; ITILE OF INVENTION: O-Fucosyltransferase	CORRESPONDENCE ADDRESS:	ADDRESSE: Genentech, inc. STREET: 1 DNA Way ; CITY: South San Francisco . CITY: California	COUNTRY: USA ZIP: 94080 COMPUTER READBLE FORM: MEDIUM TYPE: 3.5 inch, 1.44 MD flopby disk	COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COPERATING SYSTEM: PC-DOS/MS-DOS COPTWARE: WinPatin (Genentech) CHIDBENT ADPLICATION DATA.	APPLICATION NUMBER: US/09/774,954 FILING DATE: 30-Jan-2001 CLASSIFICATION: - UNKnown> PRIOR APPLICATION DATA:	APPLICATION NUMBER: US/08/978,741 FILING DATE: 26-NOV-1997 APPLICATION NUMBER: 08/792,498 FILING DATE: 31-JAN-1997) ATTORNEY/AGENT INFORMATION:) NAME: Svoboda, Craig G.) REGISTRATION NUMBER: 39,044 REPERRYCK/DOCKET NUMBER: Pl041Pl	TELECOMMUNICATION INFORMATION: TELEPHONE: 650/225-1489 TELEPRAX: 650/952-9881	SEQUENCE CHARACTERISTICS: SEQUENCE CHARACTERISTICS: TYPE: Nucleic Acid STRANDEDNESS: Single	TOPOLOGY: Linear ; SEQUENCE DESCRIPTION: SEQ ID NO: 5: US-09-774-954-5	Alignment Scores: 4.19e-237 Length: 11284 Pred. No.: 1979.00 Matches: 365 Percent Similarity: 100.00\$ Conservative: 0 Best Local Similarity: 100.00\$ Mismatches: 0	

us-09-774-954-2.rnpb

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APPLICANT: Wyeth
APPLICANT: Wyeth
APPLICANT: Wounts, William
APPLICANT: Mounts, William
TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
TITLE OF INVENTION: HUMAN OSTEDARTHRITIS AND HUMAN PROTEASES
FILE REPERENCE: 031896-043000 (AM 10.081)
CURRENT APPLICATION NUMBER: US/10/956,157
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TCCTACCAGAAGTACTTCAAGCTGGAGCCCCTCCAGGCTTACCATCGGGTCATCAGCTTG 181
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                                                                                                         ThrGly1leSerPheSerAlaSerTyrArgGluGlnTrpSerGlnArgPheSerProLys
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                                                         GAGGATTTCATGGAGAAGCTGGCACCCACTGGCCCCCTGAGAAGCGGGTGGCATAC
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"Sequence 9986, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Publication No. US20040241645A1
GENERAL INFORMATION:
APPLICANT: Yang Wang, Michael W. Spellman
TITLE OF INVENTION: O-Fucosyltransferase
NUMBER OF SEQUENCES: 17
CORRESPONENCE ADDRESS:
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APPLICATION NUMBER: US/09/774,954
FILLING DATE: 30-3an-2001
CLASSIFICATION: «UNKNOWN»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/978,741
FILLING DATE: 26-NOV-1997
APPLICATION NUMBER: 08/792,498
FILING DATE: 31-JAN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
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                                                                                                                                                                                                                                                                ADDRESSEE: Generated, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
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INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: Single
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US-09-774-954-7
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sequence 18161, Application US/11097143
publication No. US2005208558A1
publication No. US2005208558A1
publication No. US2005208558A1
publication No. US200520858A1
publication No. US200520858A1
publication No. US200520858A1
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Best Local Similarity:
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| Sequence 4751, Application US/10956157
| Sequence 4751, Application No. US20050118625A1
| GENERAL INFORMATION:
| APPLICANT: Wounts, William | APPLICANT: Wounts, William | TITLE OF INVENTION: NUCLEAR AND STROAKTHEATS AND HUMAN PROTEASES
| TITLE OF INVENTION: HUMAN OSTROAKTHEATS AND HUMAN PROTEASES
| FILE REFERENCE: 031896-043000 (AM 101081) | CURRENT PAPLIANON NUMBER: US/10/956,157 | |
| CURRENT FILING DATE: 2004-10-04 | NUMBER OF SEQ ID NOS: 319805 | SOFTWARE: Patentin version 3.2 |
| SEQ ID NO 4751 | LINCTH: 1506 | 
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   ; CURRENT FILING DATE: 2004-10-04; NUMBER OF SEQ ID NOS: 319805; SOFTWARE: PatentIn vergion 3.2; SEQ ID NO 9986; LENGTH: 1400; TYPE: DATE: ACCOUNTENT HOME OF THE SEQ ID NO 9986
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ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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28 eLeuGlySerLeuAlaPheAlaLysLeuLeuAsnArgThrLeuAlaValProProTrpIl 48
                             ----GlyArgPheGlyAsnGlnAlaAspHisPh
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EXPRESSION OF 10,000 OR MORE
           291 SerTyrValProGluLeuGln---GlnLeuPheLysGlyLysValLysValValSerLeu
                                                                     310 LysProGluValAlaGlnValAspLeuTyrileLeuGlyGlnAlaAspHisPhelleGly
                                                                                                                                                                                                                  |||| :::|||
1144 TCGTACTTCTGGGGATTC-----CCCAAGGAAAAGGAT 1176
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Matches:
Conservative:
Mismatches:
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TITLE OF INVENTION: DROSCHILLA GENES.
FILE REFERENCE: CLOO0728
CURRENT APPLICATION NUMBER: US/11/097,143
CURRENT APPLICATION NUMBER: 60/157,832
PRIOR APPLICATION NUMBER: 60/167,932
PRIOR FILING DATE: 1999-10-19
PRIOR FILING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: 60/161,932
PRIOR PILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: 60/164,769
PRIOR PILING DATE: 1999-11-22
PRIOR APPLICATION NUMBER: 60/164,769
PRIOR FILING DATE: 1999-11-22
PRIOR PILING DATE: 1999-11-22
PRIOR PILING DATE: 1999-11-28
PRIOR PILING DATE: 2000-02-24
PRIOR PILING DATE: 2000-02-24
PRIOR PILING DATE: 2000-02-24
PRIOR PILING DATE: 2000-02-34
PRIOR PILING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 43008
SOFTWARER FEARESEQ FOR WINGOWS VETRION 4.0
                                                                                                                                                                                                                                                                                      Sequence 18160, Application US/11097143
Publication No. US20050208558A1
GENERAL INFORMATION:
APPLICANT: Venter, J. Craig
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796.00
58.27*
42.49*
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Best Local Similarity:
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US-11-097-143-18160/c
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LENGTH: 3264
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376 CGATATAGCCTTCAGCAGGAGAAGAACGATCCAGACGAAGCCCAATTGCCACGCCAAGGAT
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202 TGGGTGGAGTATCGT-----AGGGGTGAACTGCGATCCCGTCAGGTGACGTTCAACACA
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                                                                        Length:
Matches:
Conservative:
Mismatches:
Indels:
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; TYPE: DNA
; ORGANISM: DROSOPHILA
US-11-097-143-18161
                                                                                               Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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                                                             Alignment Scores:
Pred. No.:
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Sequence 18082, Application US/11097143
Publication No. US20050208558A1
GENERAL INFORMATION:
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56.38%
42.39%
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                              Alignment Scores
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  2063 CCTGGGATCATTGGCCTTCGCCAAGGCGCTTAATCGCACCCTGATCCTGCCGCCGTGGGT 2004
                                                :003 GGAGTATCGT-----AGGGGTGAACTGCGATCCCGTCAGGTACCGTTCAACACATATTT 1950
                                                                               1829 TAGCCTTCAGCAGGAGAAGGATĆĆÁĠĄĆĄÁĠCCCAATTĠĆCACGCCÁÁĠGATĠĆĆÁÁ 1770
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rValProGluLeuGln---GlnLeuPheLysGlyLysValLysValValSerLeuLysPr 311
                                                                                                                                                 123
                                                                                                                                                                                    nProPheGlyProPheTrpAspGlnPheHisValSerPheAsnLysSerGluLeuPheTh 143
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                                                                                                                                                                                                                             143 rGlylleSerPheSerAlaSerTyrArgGluGln------TrpSerGlnArgPheSe 160
                                                                    eLysLeuGluProLeuGlnAlaTyrHisArgValIleSerLeuGluAspPheMetGluLy 88
                               68
                                                                                                                                                106 -----ValAlaAlaGlnArgSerProAsplysLysThrCysProMetLysGluGlYAs
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                                                                                                                                                                                                                                                                                                       uGluHisArgProLeuGlnLysTyrMetValTrpSerAspGluMetValLysThrGlyGl
                               eGluTyrGlnHisHisHisDysProProPheThrAsnLeuHisValSerTyrGlnLysTyrPh
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US-11-097-143-18082/c
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APPLICANT: Venter, J. Craig
APPLICANT: et al.
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
TITLE OF INVENTION: DROSOPHILA GENES.
TITLE OF INVENTION: DROSOPHILA GENES.
FILE REFERENCE: CLOOO728
CURRENT APPLICATION NUMBER: US/11/097,143
CURRENT FILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: 60/161,932
PRIOR FILING DATE: 1999-10-28
PRIOR FILING DATE: 1999-11-12
PRIOR FILING DATE: 1999-11-12
PRIOR FILING DATE: 1999-11-28
PRIOR FILING DATE: 1999-11-28
PRIOR FILING DATE: 1999-11-28
PRIOR FILING DATE: 1999-11-28
PRIOR FILING DATE: 2000-01-12
PRIOR FILING DATE: 2000-03-24
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Matches:
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Mismatches:
Indels:
Gaps:
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TYPE: DNA ORGANISM: Homo sapiens
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Best Local Similarity:
          US-09-918-995-19437
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LENGTH: 479
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                                                                    201 GCCACTTCATTTTGATGTGCATGCAAGGCTGCCAAGTGGCAGACCAATATCC 142
                                                                                                    160 rProLysGluHisProValLeuAlaLeuProGlyAlaProAlaGlnPheProValLeuGl 180
                                                                                                                                                      180 uGluHisArgProteuGlnLysTyrMetValTrpSer-AspGluMetValLysThrGlyG 200
                                                                                                                                                                                                          200 luAlaGlnIleHisAlaHisLeuValArgProTyrValGlyIleHisLeuArgIleGlyS 220
nProPheGlyProPheTrpAspGlnPheHisValSerPheAsnLysSerGluLeuPheTh 143
                261 TCCTTTTGGTCCCTTTTGGGACACTTTTCACATAGACTTTGTGGGGTCAGAGTTCTATGC 202
                                                                                                                               82
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USEJUL 18169, Application US/11097143

Publication No. US200502085581
GENERAL INFORMATION:

APPLICANT: et al.,
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: DESCOPHILA GENES.

TITLE OF INVENTION: DROSOPHILA GENES.

FILE REPREBRICE: CL000728

CURRENT APPLICATION NUMBER: US/11/097,143

CURRENT PILING DATE: 1999-10-05

PRIOR FILING DATE: 1999-10-05

PRIOR FILING DATE: 1999-10-19

PRIOR FILING DATE: 1999-10-28

PRIOR PILING DATE: 1999-10-28

PRIOR PILING DATE: 1999-11-12

PRIOR PILING DATE: 1999-11-12

PRIOR PILING DATE: 1999-11-12

PRIOR PILING DATE: 1999-10-28

PRIOR PILING DATE: 1999-11-12

PRIOR PILING DATE: 1999-11-12

PRIOR PILING DATE: 2000-01-12

PRIOR APPLICATION NUMBER: 60/175,693

PRIOR PILING DATE: 2000-01-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR PHILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
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Sequence 19437, Application US/09918995
Publication No. US20030073623A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                      214 IleHisLeuArg11eGlySerAspTrpLysAsnAlaCysAlaMetLeuLysAspGlyThr 233
                                                                                                                                                                                                                                                                                                                                                                                                                                        254 ProleuThrMetThrMetCysLeuProAspLeuLysGluileGlnArgAlaVallysLeu 273
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: 60/191,637
PRIOR FILING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 43008
SOFTWARE: RaceEEQ for Windows Version 4.0
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; ORGANISM: DROSOPHILA
US-11-097-143-18169
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Search completed: October 26, 2005, 15:59:38 Job time : 1594.35 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.	OM protein - nucleic search, using frame_plus_p2n model Run on: October 26, 2005, 05:59:38; Search time 6375.13 Seconds (without alignments) 2179.320 Million cell updates/sec	4-2 SYLLYCPCMGR.	Ygapop 10.0, Ygapext 0.5 Fgapop 6.0, Fgapext 7.0 Delop 6.0, Delext 7.0 Searched: 34239544 seqs, 19032134700 residues Total number of hits satisfying chosen parameters: 68479088	lengt lengt Min Max List	Command line parameters: -MODEL=frame+ p2n.model -DEV=xlh -Q=/Cgn2_1/USFTO_spool h/US09774954/runat_25102005_105432_6406/app_query.fasta_1.917 -Q=/Cgn2_1/USFTO_spool h/US09774954/runat_25102005_105432_6406/app_query.fasta_1.917 -DB=EST -QFWN=fastap -GFFTX=xrs -MINATCH=0.1 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -TRR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFWT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -USER=USOPT+4954 GCGN 1 = 5334 @FUNDA 25102005_105432_6406 -NCPU=6 -ICPU=3	-DEV_TIMEOUT=120 -WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7 :YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7 Database : EST:* 1: gb_est1:* 2: gb_est2:* 3: gb_est2:* 4: qb_est3:* 4: qb_est3:*	5: gb_est4:* 6: gb_est5:* 7: gb_est5:* 8: gb_sss1:* 9: gb_gss1:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	* Result Query No. Score Match Length DB ID	1 1979 100.0 1555 3 CR617950 CR617950 full-leng AK081059 Mus muscu 2 1832 92.6 3611 3 AK081059 AK081059 Mus muscu 4 1525 77.1 1141 5 BX353274 BX353277 S 80.1 5 BP144264 BP144264 BP144264 BP1410783 60264355 6 8 1350.5 68.5 947 4 B1410783 B1244031 BQ964179 AGENCOURT BQ964179 AGENCOURT

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/fissue_type="T cells (Jurkat cell line)
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Mus musculus adult retina cDNA, RIKEN full-length enriched library, clones A930028F21 product:protein O-fucosyltransferase 1, full insert sequence.
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                                                                                                                                                                                                                                                                                                                                                                   Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIRSN), Laboratory for Genome Exploratory Research (RIRSN), Laboratory for Genome Exploration Research Group, RIKBN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, WRL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
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GB|NM_080463, evidence: BLASTN, 99%, match=1290)
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Please visit our web site for further details.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/.
URL:http://fantom.gsc.riken.jp/.
Location/Qualifiers
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34. _1215
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                                                                                                                                                                                              /note="unnamed protein product; protein
O-fucosyltransferase 1 (MGD|MGI:2153207, GB|NM_080463,
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

ALC (bases 1 to 2616)

Adachi, A. Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Harac, A., Hashizune, M., Haracha, Hashizune, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishi, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kayach, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Kayach, H., Kuihara, C., Matsuyama, T., Miyazaki, A., Ohno, M., Ohasto, N., Okazaki, Y., Saito, R., Saitch, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shiraki, T., Takaku-Akahira, S., Sano, H., Sasaki, D., Shibata, K., Shiraski, T., Takaku-Akahira, S., Sapabe, Y., Tanaka, T., Tomaru, A., Taya, T., Yasunishi, A., Takahashi, P., Takaku-Akahira, S., Suhitet Submission Hayashizaki, Y., Toya, T., Yasunishi, A., Direct Submission Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, Wh. Jiray-v was prenared and seminanced in Monne Genome
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                                                                                                                                                                                                                                                                                                                                                            Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Pujiwake, S., Inoue, K., Tagawa, M., Ohara, E., Warahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. Rika, M., Murahiki, M., Mu
                                                                                                                                                                                                                                    genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The RIKEN Genome Exploration Research Group Phase II Team and the PANTOM Consortium. Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)
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Retina RNA was provided by Dr. Stefano Gustincich (Department of Neurobiology, Harvard Medical School, 220 Longwood Ave., Boston, 02115, USA) whose assistance is gratefully acknowledged. Please visit our web site for further details.
URL:http://ganome.gac.riken.jp/
URL:http://fantom.gac.riken.jp/
Location/Qualifiers
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                                                                                                                                              Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Komo, H., Okzaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new 9 genome Res. 10 (10), 1617-1630 (2000)
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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10349636

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ProLysGluHisProValLeuAlaLeuProGlyAlaProAlaGlnPheProValLeuGlu 180
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                                                                                                                                                                                                                                                                               MetProAlaGlySerTrpAspProAlaGlyTyrLeuLeuTyrCysProCysMetGlyArg
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 1141)

1. (contact: Genoscope consister, Meb. 91057 EvRY cedex - FRANCE Email: seqref@genoscope.cns.fr. Web: www.genoscope.cns.fr. Benish: seqref@genoscope.cns.fr. Web: www.genoscope.cns.fr. st. strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BX353274 Lomo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens cDNA clone CSODC003YJ11 5-PRIME, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                   243 GlnCysValGlyTyrSerArgSerThrAlaAlaProLeuThrMetThrMetCysLeuPro
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                                                                                     LysAsnAlaCysAlaMetLeuLysAspGlyThrAlaGlySerHisPheMetAlaSerPro
                                                                                                          LysValLysValValSerLeuLysProGluValAlaGlnValAspLeuTyrIleLeuGly
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/mol_type="mRNA"
/db_xref="taxon:9606"
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PheVallysArgGluhrgAsp---LeuGlnGlyArg------ProSerSerPhePhe 353
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                             AlaAspHisPheLeuGlySerLeuAlaPheAlaLysLeuLeuAsnArg 40
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|ProProTrp1|eG|uTyrG|nHisHisLysProProPheThrAsnLeu
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6 6 6 6

1 MetProAlaGlySerTrpAspProAlaGlyTyrLeuLeuTyrCysProCysMetGlyArg 20

US-09-774-954-2 (1-365) x BM909055 (1-1091)

Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:

1.14e-140 1394.00 79.78% 78.17%

Score:
Percent Similarity:
Best Local Similarity:
Query Match:
DB:

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Mus musculus (house mouse)
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Musculus
I (bases 1 to 947)
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602963556F1 NCI_CGAP_Lu33 Mus musculus cDNA clone IMAGE:5119332 5',
mRNA sequence.
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                                                                                                    ValLeuAlaLeuProGlyAlaProAlaGlnPheProValLeuGluGluHisArgProLeu
                           243 TCCTTCAGTGCCTCCTACAAAGACCAGTGGATCCAAAGATTTTCTCCAAAGAACATCCA
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/mol_type="mRNA"
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High quality sequence stop: 919.
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Bukaryota; Metazoa; Chordata; Craniata; Suina; Suidae; Sus.

Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

1 (bases 1 to 801)

Uenishi,H., Eguchi,T., Suzuki,K., Sawazaki,T., Toki,D., Shinkai,H., Okumuza,N., Hamashaa,N. and Awata,T.

PEDE (pig EST Date Explorer): construction of a database for ESTs derived from porcine full-length cDNA libraries

Nucleic Acids Res. 32 (1), D484-D488 (2004)

Nucleic Acids Res. 32 (1), D484-D488 (2004)

Nucleic Acids Res. 32 (1), D484-D688 (2004)

Nucleic Acids Res. 32 (1), D484-D688 (2004)

Nucleic Acids Res. 32 (1), D484-D688 (2004)

Fontact: Hirohide Uenishi
Animal Genome Laboratory, Genome Research Department
National Institute of Agrobiological Sciences

2 Ikenodai, Tsukuba, Ibaraki 305-8602, Japan

Tel: +81-29-818-8627

Fax: +81-29-818-8627

Email: huenishi@affrc.go.jp

EST project with full-length enriched cDNA libraries carried out in Animal Genome Research Program (Japan) by National Institute of Agrobiological Sciences and STAFF-Institute

Single pass sequencing of clones derived from oligo-capped cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vector sequences were eliminated by RepeatMasker version 2002/07/13 and crossmatch version 0.990319

Low quality bases were trimmed based on the quality values.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Sus scrofa"
/mol_type="mRNA"
/db xref="taxon:9823"
/clone="0VR010034G09"
/tissue_type="adult"
/dev_stage="adult"
/clone_lib="full-length enriched swine cDNA library, adult
                                                                                                      BP144264 full-length enriched swine cDNA library, adult ovary Sus scrofa cDNA clone OVR010034G09 5', mRNA sequence.
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          1028 GCAATGGGAAAGGCCCCCC 1046
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BI524031.1 GI:15348823
                                                                                                                                oGlnCysValGlyTyrSerArgSerThrAlaAlaProLeuThrMetThrMetCysLeuPr 262
                                                                             1 MetProAlaGlySerTrpAspProAlaGlyTyrLeuLeuTyrCysProCysMetGlyArg 20
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Tissue Procurement: Dr. David Rowe CDNA Library Preparation: Invitrogen Corp CDNA Library Preparation: Invitrogen Corp CDNA Library Arrayed by: The I.M.AG.E. COMSOLTIUM (LLNL) CONS Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.lln.gov column: 24
High quality sequence stop: 702.
Location/Qualifiers
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                                                     21 PheGlyAsnGlnAlaAspHisPheLeuGlySerLeuAlaPheAlaLysLeuLeuAsnArg
                                                                     147 TTTGGGAACCAGGCCGATCACTTCTGGGCTCTCTGGCATTTGCAAAGCTGCTAAACCGT
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AGENCOURT 10055799 NIH_MGC_134 Mus musculus cDNA clone IMAGE:6509783 5', mRNA sequence.
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Mammalia, Eutheria; Primates; Catarrhini, Hominidae, Homo.

Eli, M.B., Gruber, C., Jessee, J. and Polayes, D.

Full.length cDNA libraries and normalization

On May 5, 2003 this sequence version replaced gi:30377055.

Contact: Genoscope - Centre National de Sequencage

Genoscope - Centre National de Sequencage

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

Email: segrefégenoscope.cns.fr, Web: www.genoscope.cns.fr

1st strand CDNA was primed with a Not1-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and ECCR V sites of the provisors of everor. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSOAJOOBDCO6CPI&c=9980.f.

Location/Qualifiers

irce | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 | 1841 
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BX345989. GI:46549776
                                                                                                                                                                   LysAsnAlaCysAlaMetLeuLysAspGlyThrAlaGlySerHisPheMetAlaSerPro 242
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US-09-774-954-2 (1-365) x BX345989 (1-841)

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AGENCOURT 10032510 NCI CCAP Mam2 Mus musculus cDNA clone IMAGE:6485896 5', mRNA sequence.
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Mus musculus (house mouse)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 915)
NIH-MGC http://mgc.nci.nih.gov/.
NIH-MGC http://mgc.nci.nih.gov/.
Ontact: Robert Strausberg, Ph.D.
Email: Gapba: "Gmall.nih.gov
Tissue Procurement: Glibert Smith, Ph.D.
Tissue Procurement: Glibert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
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815 242 875

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Homo sapiens (Human)

Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 898)

1 (Lases 1 to 898)

1 (Lases 1 to 808)

1 (Lases 1 to 808)

2 ii, W.B., Gruber, C., Jessee, J. and Polayes, D.

1 (Published (2001)

1 (Dablished (2001)

2 on May 22, 2003 this sequence version replaced gi:31030014.

Contact: Genoscope - Centre National de Sequencage

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr

1 st strand cDNA was primed with a NotI-014go(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.

This sequence belongs to sequence cluster 9980.f

For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CSOAM014AF06QP1&c=9980.f.
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/dev_stage="FETAL"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BX449172 Homo sapiens FETAL LIVER Homo sapiens cDNA clone CSODM014YK11 5-PRIME, mRNA sequence.
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816 AAGAATGCCTGTGGCATGCTGAAGGATGGAACTGCAGGGTCACACTTCATGGCCTCCCT
                                                                                                                     LysAsnAlaCysAlaMetLeuLysAspGlyThrAlaGlySerHisPheMetAlaSerPro
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Conservative:
Mismatches:
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BX449172.2 GI:47067286
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65.89%
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AUTHORS
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BX449172
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Site_2: Not1; Cloned unidirectionally. Primer: Öligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   635
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  183 ArgProLeuGlnLysTyrMetValTrpSerAspGluMetValLysThrGlyGluAlaGln 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         215
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                Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLANLORO g column: 17
Plate: LLANLORO sequence stop: 698.
High quality sequence stop: 698.
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Pred. No.:
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AlaTyrCysPheGluValAlaAlaGlnArgSerProAspLysLysThrCysProMetLys 120
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                                                                                                                                                                                                                                                                                                                                                                                                                              LeuPheThrGlyIleSerPheSerAlaSerTyrArgGluG1nTrpSerG1nArgPheSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITITIACAGGCAITITCCTICAGTGCTTCCTACAGAACAATGGAGCCAGAGATTTTCT
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/locle=lib="fatze MNLV"
/note=organ: liver; Vector: pDONR 222; Site_1: BsrG
Site_2: BsrG I; Created from CloneMiner cDNA_Library
Construction kit (catalog #18249-029)"
                                                                                                                                                                                                                                                                                                        942
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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|strain="Indian"
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|clone="IBIUW:29960"
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BACKARAD: CACTATAGGGGGAATGGGTA
Insert Length: 942 Std Brror: 0.00
Plate: CL000531 row: E column: 09
Seg primer: CCCTCACTAAAGGGAACAAAA
POLYA-NO.
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                                                                                 Location/Qualifiers
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92.11%
65.89%
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Best Local Similarity:
Query Match:
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CO774833 G:0774833. G:50976096
EST.
Macaca nemestrina (pig-tailed macaque)
                                                                                                                                                                                                                       140
                                                                                                                                                                                                                                                                                                                                                                                        161 ProLysGluHisProValLeuAlaLeuProGlyAlaProAlaGlnPheProValLeuGlu 180
                                                                                                                                                                                                                                                                                                                                                                                                                                               rAspTrpLysAsnAlaCysAlaMetLeuLysAspGlyThrAlaGlySerHisPheMet-A 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fax: 2063780408
Email: cmagness@illumigen.com
Sequenced on 2004.07.21. 611 020 bases. Library Preparation: Prof.
Michael Katze Lab at University of Washington DNA Sequencing:
Illumigen Biosciences Inc. For further information, see
http://www.macaque.org
                                                                                                                                                                                                                                                                               160
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                                                                                                                             101 AlaTyrCysPheGluValAlaAlaGlnArgSerProAspLysLysThrCysProMetLys 120
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1 (bases 1 to 942)

Katze,M.G., Thomas,M., Korth,M., ladonato,S.P. and Magness,C.L. Large-scale Rheeus Macaque cDNA Sequencing
Umpublished (2003)

Contact: C. Magness

Illumagen Biosciences Inc.

2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
   9
                                                      80
                                                                         SerLeuGluAspPheMetGluLysLeuAlaProThrHisTrpProProGluLysArgVal
                                                                                                                                                                                      439 GCATACTGCTTTGAGGTGGCAGCCCAGCGAAC-CCAGATAAGAAGACGTGCCCCATGAAG
                                                                                                                                                                                                                          GluGlyAsnProPheGlyProPheTrpAspGlnPheHisValSerPheAsnLysSerGlu
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    ThrieuAlaValProProTrpIleGluTyrGlnHisHisLysProProPheThrAsnLeu
                                                        HisValSerTyrGlnLysTyrPheLysLeuGluProLeuGlnAlaTyrHisArgVallle
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602705255F1 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:4842061 5', mRNA sequence.
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CITITIACAGGCATITCCTTCAGTGCTTCCTACAGAGAACAATGGAGCCAGAGATTTTCT 121
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 808)
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                                                                          ccaaaggaacarcccgrccrrcccrcccagaaccccagrrccccagrrccccarcragag
                                                                                                                                       AspTrpLysAsnAlaCysAlaMetLeuLysAspGlyThrAlaGlySerHisPheMetAla
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                                                                                                                    GluHisArgProLeuGlnLysTyrMetValTrpSerAspGluMetValLysThrGlyGlu
                                                                                                                                                                                                                      GCCCAGATTCATGCCCACCTTGTCCGGCCCTATGTGGGCATTCATCTGCGCCATTGCTTCT
                                                                                                                                                                                                 AlaGlnIleHisAlaHisLeuValArgProTyrValGlyIleHisLeuArgIleGlySer
                                       ProLygGluHisProValLeuAlaLeuProGlyAlaProAlaGlnPheProValLeuGlu
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   341 ArgGluArgAspLeuGlnGlyArgProSerSerPhePheGlyMetAspArgProPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution: MGC clone distribution at: found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLCM1675 row: n column: 14 High quality sequence stop: 808.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC

    .808
    /organism="Homo sapiens"
    /mol_type="mRNA"

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DKFZp76200115_r1 762 (synonym: hmel2) Homo sapiens cDNA clone

DKFZp76200115_s', mRNA sequence.

AL135434
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1 (Dases 1 to 719)
Ansorge, W., Wirkner, U., Mewes, W., Weil, B. and Wiemann, S.
EST (Ansorge, W., Wirkner, U., Mewes, H.W., Weil, B. and Wiemann, S.)
Unpublished (1999)
Contact: MIPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genme Analysis, German Cancer
Research Center (DKE2); Email s. Wiemann@dkfz- heidelberg.de;
sequenced by EMBL (Buropean Molecular Biology Laboratories,
Heidelberg/Germanny) within the cDNA sequencing consortium of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 GAAGGAAACCCCTTTGGCCCATTCTGGGATCAGTTTCATGTGAGTTTCAACAAGTCGGAG
  GCCCAGAATCCCGCCCACCTTGTCCCGGCCCTATGTGGGCATTCCTCTACGTAATGGCTT
                                                              220 eraspTrpLysAsnAlaCysAlaMetLeuLysAspGlyThrAlaGlySerHisPheMetA
                                                                                           240 jaSerProGlnCysValGly-TyrSerArgSerThrAlaAla-ProLeuThrMetThrMe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              German Genome Project.

No 81 sequence available.
This clone (NKPZp76200115) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 1405;
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sall"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone lib="762 (synonym: hmel2)"
/note="Vector: pSport1; Site_1: Not1; Site_2:
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/db_xref="taxon:9606"
/clone="DKPZp76200115"
/clssue_type="melanoma (MeWo cell line)"
/dev stage="adult"
/lab_host="DH108"
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Mismatches:
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Query Match:
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/db_xref="taxon:9606"
/clone="InfAGE:4842061"
/clone="InfAGE:4842061"
/lab_host="normal pigmented retinal epithelium"
/lab_host="normal pigmented retinal epithelium"
/lab_host="normal pigmented resistant)"
/clone=lib="NNH MGG 43"
/note="Organ: eye; Vector: poTB7; Site 1: Xho1; Site 2:
EcoR1; cDNA made by oligo-dT priming. Directionally
cloned into EcoMAT/Aho1 sites using the following 5;
adaptor: GGCACAGG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis Kit
(Stratagene) and Superscript II; (Life Technologies).
Note: this is a NIH_MGC Library. |"
                                                                                                                                                                                                                                                                                                                                  LeuBheThrGly11eSerPheSerAlaSerTyrArgGluGlnTrpSerGlnArgPheSer 160
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                                                                                                                              Length:
Matches:
Conservative: 1
Mismatches: 5
Indels: 0
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Search completed: October 26, 2005, 15:17:12 Job time : 6398.13 secs us-09-774-954-2.rpr

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

October 25, 2005, 15:21:43; Search time 45.7187 Seconds (without alignments) 768.157 Million cell updates/sec Run on:

US-09-774-954-2 1979 1 MPAGSWDPAGYLLYCPCMGR......QGRPSSFFGWDRPPKLRDEF 365 Title: Perfect score: Sequence:

Scoring table:

283416 seqs, 96216763 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	hypothetical prote	F20D23.3 protein -	hypothetical prote	_	hypothetical prote	reverse transcript	hypothetical prote	probable magnesium	mucin A, tracheal	hypothetical prote	self-incompatabili	able serin	p97 protein - Toxo	branched-chain-ami	transforming prote	nitrate reductase	tryptophan synthas				parasporal crystal	cryptic nitrate re		class I histocompa	_	hypothetical prote			probable transamin
	ID	T15511	A86309	T14795	S07624	T37509	T31657	G83690	T31462	146225	F59099	S37459	T38692	T03098	T40454	T04869	G64899	D95211	F91080	G85925	T29439	S00944	G90887	B85730	839599	AI2421	T47393	JC4655	7	E69168
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	Lengt	47	5	383	73	43	1209	458	1292	44	43	21	650	87	38	427	1246	407	520	520	49	1189	1246	124	328	77	42	73	82	41
,	Query Match Length	27.4	5.8	5.3	5.1	4.9	4.8	4.7	4.6	4.6	4.5	4.5	4.5	4.5	4.4	4.4	4.4	4.4	4.4	4.4	4.4	4.4	4.4	4.4	4.3	4.3	4.3	4.3	4.3	4.3
	Score	541.5	114	105.5	101.5	96.5	94.5	93.5	91.5	90.5	90	89.5	89	88.5	88	88	87.5	87	87	87	86.5		86.5		85.5		85	85	82	84.5
	Result No.	7	8	e	4	Ŋ	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

1117 2 AE0075 283 2 844848 390 2 884848 390 2 864811 4400 2 T33758 145 1 E64096 349 1 E64096 554 2 AE2088 1242 2 AE0072 263 2 JH0635 534 2 P96713 659 2 AB1293 653 2 B81123	polyketide synthas hypothetical prote KO6H7.8 protein - KO9CH6.10 protein - KO9CH7.10 protein - KO9CH6.10 protein - KO9CH7.10 protein	ABC transporter (p hypothetical prote lipopolysaccharide
200109873 200108973 2008973 3008483 200777 20077	S43048 AE0075 S86414 UC7387 T133758 AH2479 E64096 S67452 AB2088 AB0672 JH06335 P96713	AB1293 T20226 B81037
	3519 2 2813 2 2 390 2 2 255 2 2 255 2 2 263 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	659 2 623 2 623 2
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	8 8888 894 4 8 6 8 8 6 7 7 7 8 8 8 8 8 9 7 7 7 8 8 8 8 8 8 7 7 7 8 8 8 8	8 2 2 2 2 8 3 2 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3
	0 1 2 2 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	. 4 4 4 1 W 4 D

ALIGNMENTS

RESULT 1 T15511 hypochetical protein C:Species: Caenorhab C;Accession: T15511 R;Leimbach, D. submitted to the EMB A;Description: The SA;Reference number: A;Accession: T15511 A;Status: The SA;Reference number: A;Accession: T15511 A;Catus: The SA;References: C;Genetics: T474 <la 125;="" 139="" 19="" 222="" 31="" 3;="" 67="" a;coss-references:="" a;gene:="" a;introns:="" best="" c;genetics:="" carperd<="" cesp:c15c7.1="" con="" cuery="" cy="" db="" empktg="" grfcnq="" l19="" local="" match="" matches="" qy="" selftg="" similar="" th="" vvtwqe=""><th>THE SECONT TARGET TO THE SECONT OF THE SECONT TARGET TARGE</th></la>	THE SECONT TARGET TO THE SECONT OF THE SECONT TARGET TARGE
 ' ଶ୍ର	:::: : : : 336 RITEQAKKFISANLAKPFVAVHLRNDADWVRVCEHI-DTTTNRPLFASEQCLGEGHHLGT 394
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CESP: C15C7.

RESULT 2 A86309 F20023.3 protein - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) 셤

395 -LTKELCSPSKQQI-----LEQ------IEAHRQEPDD 420

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314 AQVDLYILGQADHFIGNCVSSFTAFVKRERDLQG---RPSSFFGM 355

254 PLIWIMCLPDLKEIQRAVKLWVRSLDAQSVYVATDSESYVPELQQLFKGKVKVVSLKPEV 313

N

160

91

- PLOKYMVWSDEMVKTGEAQIHAHL 207

-----QDVPSLEGA 315

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132 SGGPFIDQV-YVLQSYAE-----GWKEGTWEEKVDERPCIDQLLYSQDKHEYYRGWF 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            208 VRPYVGIHLRIGSDWKNACAMLKDGTAGSHFWASPQCVGYSRSTAAPLTMTMCLPDLKEI 267
                                                                                                                                                                                                   92 THWPPEKRVAYCFEVAAQRSPDKKTCPMKEGN----PFGPFWDQFHVSFNKSELFTG-- 144
                                                                  -----YLLY--CPCMGRFGNQADHFLGSLAFAK 36
                                                                                                         16 AVSWPPASASGQEFWPGQSAADILSGAASRRRYLLYDVNPPEG-FNLRRDVYIRIASLLK
                                                                                                                                                            37 LINRT----LAVPPWIEYQH-HKPPFTNLHVSYQKYFKLEPLQAYHRVISLEDFWEKLAP
                                                                                                                                                                                                                                                                                                                                                                                       183 WGYEETRGLNVSCLSVQGSASIVAPLLLRNTSARSVMLDRAENLLHDHYGGKEYWDTRRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . Similarity 21.1%; Pred. No. 0.32;
87; Conservative 42; Mismatches 126; Indels 157; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              288 GGPYLGVHLR------RKDFIWGHR----
                                                                                                                                                                                                                                                                                                                                                     145 ------ISFSASY------
                                                                                                                                                                                                                                                                                                                                                                                                                                            161 PKEHPVLALPGAPAQFPVLEEHR------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A Status: translation not shown A Molecule type: DNA Residues: 1-732 cLIN> A Cross-references: EMBL:X14915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 22.9% tes 81, Conservative
          Best Local Similarity
Matches 87; Conserv
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Best Local S
Matches 81
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C; Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C; Accession: A86309
R; Theologis, A.; Ecker, U.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, W.K.; Com, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
A; Huther 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Liu, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, A; Rooney, T.; Rowaley, D.; Sakano, H.; Shun, P.; Southwick, A.M.; Sun, H.; Tallon, A; Atthors: Salzberg, S.L.; Schwarz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A; Telle: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Accession: A86309
A; Accession: A86309
A; Asterius: preliminary
A; Molecule type: DNA
A; Residues: 1-594 <STO>A; Residues: 1-594 <STO>A; Residues: 1-594 <STO>A; Rossicules: UNIPROR: Q98HIS; GB: AE005172; NID: G5734743; PIDN: AAD50008.1; GSPDB:GN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    354 DGVIAIGDVFYADMEQDLVWQPGGFINHXCKTLIEPBRLILVTAQRFIQT-----FLG 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HVSYQKYPKLEPLQ---AYHRVISLEDFMEKLAPTHWPPEKRVAYCFEVAAQRSPDKKTC 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          258 ---YDKVIDIERINTCLGRTVVISFDQFKE-----IDKKNNAHI-------DRFIC 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .---- 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----FSPKEHPVLALPGAPAQFPVLEEHRPLOKYMVWSDEMVKTGEAQIHAHLV 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           209 RPYVGIHLR---IGSDWKNACA----MLKDGTAGSHFWASPQ----CVGYSRSTAAPLIM 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      407 KNPISLHLRRHGFLKFWLQNLAIVAIMYLDSVAHTQLIGIPEHLSTCNAKSPS----- 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   258 IMCLPDLKEIQRAVKLWVRSLDAQSVYVATD-SESYVPELQQLFKGKVKVVSL---KPE- 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             460 -- CFYPIPQAADCISRMVERANAPVIÝLSTĎAAEŠETGLLÖSĽVVVDGKVVPĽVKRPPQN 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----- 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 WDP-AGYLLYCPCMGRFGNQADHFL---GSLAFAKLLNRTLAVP-PWIEYQHHKPPFTNL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SABKWDSLLYRHGIEDDSQVYAMLDKTİCAMSSVFİĞASGSTFTEDILRLKKDWĞTSS 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----VAQVDLYILGQADHFIGNCVSSFTAFVKRERDLQGRPS 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypochetical protein DKFZp434B171.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Species: 20-Sep1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T14795
R;Poustka, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
B;Poustka, A.; Klein, M.; Mewes, Batabase, August 1999
A;Reference number: Z18183
A;Accession: T14795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
5.8%; Score 114; DB 2; Length 594;
Best Local Similarity 20.1%; Pred. No. 0.1;
Matches 84; Conservative 50; Mismatches 160; Indels 124;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           209 WKPRPDKFLFAICLS--GQMSNHLICLEKHMFFAALLDRVLVIPSSKFDYQ--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               118 PMKEGNPFGPFWDQFHVSFNKSELFTGISFSASYREQWSQR------
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A;Experimental source: adult testis; clone DKF2p434E171
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A;Molecule type: mRNA
A;Residues: 1-383 <POU>
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acylaminoacyl-peptidase (EC 3.4.19.1) - rat
acylaminoacyl-peptidase (EC 3.4.19.1) - rat
acylaminoacyl-peptidase (EC 3.4.19.1) - rat
NyAlternate names: acyl-peptide hydrolase; acylamino-acid-releasing enzyme
N;Alternate names: acyl-peptide hydrolase; acylamino-acid-releasing enzyme
C;Specises: Rattus norvegicus (Norway rat)
C;Specises: Rattus norvegicus (Norway rat)
C;Accession: A3706; 807624
R;Kobayashi, K.; Lin, L.W.; Yeadon, J.E.; Klickstein, L.B.; Smith, J.A.
J.B.I. Chem. 264, 8892-8899, 1989
J. Biol. Chem. 264, 8892-8899, 1989
A;Attle: Cloning and sequence analysis of a rat liver cDNA encoding acyl-peptide hydrolas
A;Molecule: 1732 < KND
A;Accession: A33706; MUD:89285389; PMID:272805
A;Molecule: 1732 < KND
A;Accession: MANA
A;Residues: 1732 < KND
A;Accession: MANA
A;Residues: UNIPROT:P13676; GB:J04733; NID:g202931; PIDN:AAA88506.1; PID:g202932
A;Cross-references: UNIPROT:P13676; GB:J04733; NID:g202931; PIDN:AAA88506.1; PID:g202932
A;Cross-references: UNIPROT:P13676; BB:D4000
A;Rile: Structural organization of the rat acyl-peptide hydrolase gene.
A;Reference number: S0724; MUD:89296508; PMID:2578023
A;Reference number: S0724; MUD:89296508; PMID:2578023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ajintrons: 4/3; 49/1; 91/2; 122/3; 148/1; 202/3; 248/3; 279/2; 293/1; 333/3; 354/1; 386/2; Ajintrons: 4/3; acylaminoacyl-peptidase
C; Superfamily: acylaminoacyl-peptidase
C; Keywords: blocked amino end; homoterizamer; hydrolase; omega peptidase
F; 1/Modified site: blocked amino end (Met) (probably acetylated) #status experimental
F; 118, 291, 443/Modified site: lysine derivative (Lys) #status experimental
F; 587, 675, 707/Active site: Ser, Asp, His #status predicted
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22.9%; Pred. No. 1.6;
ative 32; Mismatches 101; Indels 139; Gaps
268 QRAVKLWVRSLDAQSVYVATDSESYVPELQQLFKGKVKVVSLKPEVAQVDLY 319
                                                             | :: ::: | :::| | :::| | 316 VRKIRSLMKTHRLDKVFVATDAVR--KEYBELKKLLPEMVRFEPTWEELELY 365
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RiTakani, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hiran Nucleic Acids Res. 28, 4317-4331, 2000
Apritle: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and ¿ A, Reference number: A83650, MUD:20512582; PMID:11058132
A, Accession: G83690
A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-458 < STO>
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                                               A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1209 <BIR>A;Cross-references: UNIPROT:P91581; EMBL:Z83760; NID:e1014349; PID:e289993; PIDN:CAB0604; G;Genetics:
A;Cross-references: UNIPROT:P91581, EMBL:Z83760; NID:e1014349; PID:e289993; PIDN:CAB0604; A;Note: COS41.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      290 HWPEPDSIRHMTRMAEEDHKTSVTIEKEDANIAFPRAGFGLPVIFQFHSKDRQDPFPTIL 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      196 VKTGEAQIHAHLVRPYVGIHLRIGSDWKNACAMLKDGTAGSHFWASPQCVGYSRSTAAPL 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAPLIMIMCLPDLKEIQRAVKLWVRSLDAQSVYVATDSESYVPELQQLFKGKV---KVVS 308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ------ 376
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  -AQFPVLEEHRPLQKYMVW 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SDEMVKTGEAQIHAHLVRPYVGIHLRIGSDWKNACAMLKDGTAGSHFWASPQCVGYSRST 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ------VVEAVRKWSHFLKGKSFTLVTDQRSVSFMFDQRNRGKIKNSKILM 822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypochetical protein BH0327 [imported] - Bacillus halodurans (strain C-125) C;Species: Bacillus halodurans C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004 C;Accession: G83690 R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno. G.: Saraki R. Maeni N. B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gape
                                                                                                                                                                                                                                                                                                                                                                             59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89;
                                                                                                                                                                                                                                                                                                    Length 1209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 4.7%; Score 93.5; DB 2; Length 458; 1 Similarity 18.3%; Pred. No. 4.3; 51; Conservative 50; Mismatches 89; Indels 8
                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           739 SDYAI----AAVLSQSGRPVAYMSRTLNTCERNYPAIEKEATA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               309 LKPEVAQVDLYILGQ--ADHFIGNCVSSFTAFVKRERDLQ 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : |::| |::|| 823 WRLELSQFTYDIVHRPGRDNFVPDALSRVNALNRDLKELQ 862
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                                                                                                                                                                                                                                                                                                                                                                                83;
                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                           Query Match

4.8%; Score 94.5; D:
Best Local Similarity 20.0%; Pred. No. 12;
Matches 44; Conservative 34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                         150 SYREQWSQRFSPKEHPVLALPGAP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               350 KPRGKDRLASRLI-------
Reference number: Z21049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 51; Conserv
                                    A; Accession: T31657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                192
                                                                                                                                                                                                                                                                                                                                               Best Loca
Matches
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R;Connor, R.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
submitted to the EMBL Data Library, November 1997
A;Reference number: 221719
A;Accession: T37509
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-432 <CON>
A;Residues: 1-432 <CON>
A;Experimental source: strain 972h-; cosmid c10F6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                163 EHPVLALPGAPAQFPVLEEHRPLQKYMVW---SDEMVKTGBAQIH-------A 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RSTAAPLIMIMCLPDL----KEIQRAVKLWVRSLDAQSVYVATDSESYVPELQQLFKGK 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VKVVSLKPEVAQVDLYILGQADHF-IG---NCV----SSFTAFVKRERDL--QGRPSSFF 353
                                                                                                                                                                                  217 RIGS----DWKNACAMLKDGTAGSHFMASPQCVGYSRSTAAPLITMTMCLPDLKEIQRAVK 272
       -RVISLEDFMEKLAPTHWPP-EKRVAYC---FE---VAAORSPDKKTCP---MKEGNPFG 126
                                                      174 AQFPV----LEEHRPLQKYMVWSDEMVKTGEAQIHAHLV-------RPYVGIHL 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein SPAC10F6.15 - fission yeast (Schizosaccharomyces pombe)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Ciona intestinalis
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T3165;
R;Bird, A.P.; Clark, V.; Jones, S.J.; Leitgeb, S.; Dobson, R.; Tweedie, S.
submitted to the EMBL Data Library, December 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Species: Schizosaccharomyces pombe
Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   619 MMGSTDIPDW----CMVETG------FPYSNS------CLPDL-----N
                                                                                                                                              127 PF---WDOFHVSFNKSELFTGISFS---ASYREQWSQRFSPKEHPVLALPG-----AP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   273 LWVRSLDAQSVYVATDSESYVPELQQLFKGKVKVVSLKPEVAQVDLYILGQAD 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 432;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        reverse transcriptase homolog - sea squirt (Ciona intestinalis)
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4.9%; Score 96.5; Di
Best Local Similarity 21.3%; Pred. No. 2.2;
Matches 52; Conservative 47; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: SPDB:SPAC10F6.15 A;Map position: 1
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Matches S8; Conservative 29; Mismatches 75; Indels 127; Gaps 14;	SULT 10 9109 9109 9109 90161101 Species: Bac Bacte: 12-Nov Bacte: 12-Nov Bacte: 12-Nov Bacte: 12-Nov Bacte: 10-Nov Query Match 4.5%; Score 90; DB 2; Length 437; Best Local Similarity 20.7%; Pred. No. 8; Matches 6; Conservative 35; Mismatches 136; Indels 94; Gaps 14; Qy 2 PAGSWAPAZLYCPCPMGRFGNOADHF	Qy 159 FSPKEHPVLALPGAPA-QFPVLEEHRPLQKYMVWSDEMVKTGEAQIHAHLVRPYV 212 Db 184 LMSGSPGILIPFRNQYNQIVGWQVRVDEVKNSVHVKSAPTGIQAELI 230 Qy 213 GIHLRIGSDWKNACAMLKDGTAGSHFWASPQCVGYSRSTAAPLTMTWCLPDLKEI 267 Db 231FQPNVVKTKDG	
RESULT 8 T31462 probable magnesium chelatase (EC 4.99.1) chain H BchH - Heliobacillus mobilis C;Species Heliobacillus mobilis C;Species Heliobacillus mobilis C;Species G2-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 09-Jul-2004 C;Accession: T1462 R;Xiong, J: Inoue, K.; Bauer, C.E. Proc. Natl. Acad. Sci. U.S.A. 95, 14851-14856, 1998 A;Title: Tracking molecular evolution of photosynthesis by characterization of a major F, A;Reference number: Z21036; MUID:99061957; PMID:9843979 A;Accession: T31462 A;Accession: T31462 A;Accession: T1292 < xIO> A;Molecule type: DNA A;Residues: 1-1292 < xIO> A;Molecule type: DNA A;Residues: DthH C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Keywords: lyase		I G H	C; Accession: PC1174; I46225 — C; Accession: PC1174; I46225 — C; Accession: PC1174; I46225 — C; Accession: PC1174; I46225 — C; Accession: Biochem.

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A;Molecule type: mRNA
A;Residues: 1-877 <MAT>
A;Cross-references: UNIPROT:O15644; EMBL:AF005059; NID:g2581824; PIDN:AAC47857.1; PID:g2:
A;Experimental source: strain RH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Accession: T03098
R;Matsuura, T.; Kasper, L.
Mol. Biochem. Parasitol. 90, 403-413, 1997
A;Title: Molecular analysis and characterization of a protein involved in the replication A;Reference number: Z14838; WUID:9813555; PMID:9476788
A;Recession: T03098
A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 564 -- VLFKNMVESSGASIEQTF-EEWAQSKAPSGNEWINWRRAHKGPLHEVLODPEGWKLYR 620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---RPYVGIHLRIG-----SDWKNACAMLKDGTAGSHFWASPQCVGYSRSTAAPLTWT 258
                                                                                                                                                                                                                             SEDIADSITSSTFFPVLPQIRESTPLNLKLRNFIISSSEDSTSPKAK---EFDRPLPSTE 484
                                                                                                                                                                                                                                                                                                                              93 HWP-------PEKRVAYC-----FEVAAQRSPDKKTCPMKE--GNPFGPFWDQ 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .-----HPVLALP----- 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    621 ENLVRKNVVDVPQSPEDFLQQPDQQKAAATSKWSSW------RRVHRGPLVTVLADK 671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     374 --CNTEEESRINPSTSKFLKQLNKG--FNG--FTKPFRKSKKGSKNRKNKSSVATQFSEE 427
                                                                                                                                                                                                 EHPVLALPGAPAQFPVLEEHRP-----LQKYMVWSDEMVKTGEAQIHAHLVRPYVGIH 215
                                                                                                                                                                                                                                                                                                 LRIGSDWKNACAMLKDGTAGSHFMASPQCVGYSRSTAAPLTWTMCLPDLKEIQRAVKLWV 275
                                         324 RPTAEMCLDLE------FCRVSAPADAVASKEEVNKNTDFRVSISYFPSSSSIPDE 373
PPFINLHVSYQKYFKLEPLQAYHRVISLEDFMEKLAPTHWPPEKRVAYCFEVAAQRSPDK 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------TNLHVSYQKYFKLEPLQAYHRVIS------LEDFMEKLAPT 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 p97 protein - Toxoplasma gondii
C,Species: Toxoplasma gondii
C,Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          115 KTCPMKEGNPFGPFWDQFHVSFNKSELFTGISFSASYREQWSQ-------RFSPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 DPAGYLLYCPCMGRFGNQADHFLGSLAFAKLLNRTLAVPPWIEYQH-HKPPF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----GAPAQF-----PVLEEHRPLQKYMVWSDEMVKTGEAQIH-AHLV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gondii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.5%; Score 88.5; DB 2; Length 877;
19.9%; Pred. No. 27;
tive 44; Mismatches 119; Indels 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Function:
A;Description: involved in replication of intracellular Toxoplasma
C;Superfamily: Toxoplasma gondii p97 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    132 FHVSFNKSELFTGISFSASYREQWSQRFSPKE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                      276 RSLDAQSVYVATDSESYVP 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 19.9%
Matches 74; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : || :::|
725 LADPDGWDLYKA 736
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     22
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A;Experimental source: strain LA 2157; style tissue
A;Note: submitted to the EMBL Data Library, September 1993
A;Note: part of this sequence, including the amino end of the mature protein, was determ
A;Note: part of this sequence, including the amino end of the mature protein, was determ
A;Note: part of this sequence, including the amino end of the mature protein,
C;Keywords: angiosperm reproduction; glycoprotein
F:1-17/Domain: signal sequence (fragment) #status predicted <SIG>
F:18-218/Product: self-incompatability glycoprotein #status predicted
F:46,56/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Mosidues: 1-650 <BRO>
A;Kosidues: 1-650 <BRO>
A;Kosidues: 1-650 <BRO>
A;Cross-references: UNIPROT:014132; EMBL:Z99568; PIDN:CAB16737.1; GSPDB:GN00066; SPDB:SF
A;Experimental source: strain 972h-; cosmid c3C7
                                                                                                     C,Accession: 837459
R;ROyo, J.; Kunz.
C.; Kowyama, Y.; Anderson, M.; Clarke, A.E.; Newbigin, E.
Proc. Natl. Acad. Sci. U.S.A. 91, 6511-6514, 1994
A;Title: Loss of a histidine residue at the active site of S-locus ribonuclease is assoch Accession: 837459
A;Accession: 837459
A;Nolecule type: mRNA
A;Residues: 1-218 <ROX>
                                                    self-incompatability glycoprotein, mutant non-functional allele - Peruvian tomato (fragm
C,Species: Lycopersicon peruvianum (Peruvian tomato)
C,Date: 06-Jan-1995 #sequence_revision 31-Jan-1997 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probable serine/threonine-specific protein kinase (EC 2.7.1.-) SPAC3C7.06c [similarity] C.Species: Schizosaccharomyces pombe C.Species: 03-Dec-1999 #text_change 16-Aug-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 VSYQKYPKLEPLQAYHRVISLEDFWEKLAPTHWPPEKRVAYCFEVAAQRSPDKKTCPMKE 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 GNPFGPFWDQFHVSFNKSELFTGISFSASYREQWSQRFSPKEHPVLALPGAPAQFPVL-- 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EEHRPLOKYMVWSDEMVKTGEAQIHAHLVRPYVGIHLRIGSDWKNACAMLKDGTAGSHFM 239
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R;Brown, D.; Churcher, C.M.; Wood, V.; Barrell, B.G.; Rajandream, M.A.
Submitted to the EMBL Data Library, September 1997
A;Reference number: Z21805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 4.5%; Score 89.5; DB 4; Length 218; Local Similarity 19.4%; Pred. No. 3.6; es 45; Conservative 43; Mismatches 103; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
4.5%; Score 89; DB 2; Length 650;
Best Local Similarity 22.3%; Pred. No. 16;
Matches 71; Conservative 50; Mismatches 126; Indels
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C;Keywords: phosphotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A, Gene: SPDB:SPAC3C7.06c
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Matches
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                                                                                          C; Species: Schizosaccharomyces pombe
C; Date: 03-Dec-1999 #squaremore revision 03-Dec-1999 #text_change 09-Jul-2004
C; Date: 03-Dec-1999 #squaremore revision 03-Dec-1999 #text_change 09-Jul-2004
C; Date: 03-Dec-1999 #squaremore revision 03-Dec-1999 #text_change 09-Jul-2004
C; Date: 03-Dec-1999 #squaremore revision 03-Dec-1999 #text_change 09-Jul-2004
C; Date: 03-Dec-1999 #squaremore revision 03-Dec-1999 #text_change 09-Jul-2004
R; Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Baker, S.; Mungall, K.
A; Reference mumber: Z21931
A; Residues: 1-380 < LXN;
A; Residues: 1-380 < LXN;
A; Residues: 1-380 < LXN;
A; Residues: 1-380 < LXN;
A; Residues: 1-380 < LXN;
A; Residues: 1-380 < LXN;
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A; Residues: Residues: Robert Robert Robert Robert Robert Robert Robert Robert Robert Robert Robert Robert Robert Robert Robert Robert Robert Robert Robert Robert Robert Robert Robert Robert Robert Robert Robert Robert Robert Robert Robert Robert Robert Robert Robert Robert Robert Robert Robert Robert Robert Robert Robert Robert Robert Robert Robert Robert Robert Robert Robert Robert Robert Robert Robert Robert Robert Robert Robert Robert Robert Robert Robert Robert Robert Robert Robert Robert Robert Robert Robert Robert Robert Robert Robert Robert Robert Robert Robert Robert Robert Robert Robert Robert Robert Robert Robert Robert Robert Robert Robert Robert Robert Robert Robert Robert Robert Robert Robert Robert Robert Robert
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Dates: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 16-Aug-2004
C;Dates: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 16-Aug-2004
R;Beran, M; Mueller, M.W.; Muendlein, A.; Felber, R.; Bancroft, I.; Mewes, H.W.; Mayer, A;Reference number: Z15387
A;Reference number: T04869
A;Reference number: DNA
A;Rodecule trpe: DNA
A;Residues: 1-427 <BEV>
                                                                branched-chain-amino-acid transaminase (EC 2.6.1.42) precursor, mitochondrial - fission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  172 APAQFPVLEEHRPLQKYMVWSDEMVKTG-----EAQIHAHLVRPYV----- 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          213 ---GIHLR---IGSDWKNACAMLKDGTAGSHFMASPQCVGYSRSTAAPLTMTMCLPDLKE 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         144 RGYSLYIRPTFIGTD--EALGVHHCDNAMLXVIASPVGPYYSSGFKA---VKLCCS---- 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52 HHKPPFTNLHVSYQKYFKLEPLQAYHRVISLEDFMEKLAPTHWPPEKRVAYCFEVAAQRS 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         112 PDKKTCPMKEGNPFGPFWDQFHVSFNKSELFTGISFSASYREQWSQRFSPKEHPVLALPG 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        267 IQRAVKLWVRSLDAQSVYVATDSESYVPELQQLFKGKVKVVSLKPEVAQVDLYILGQADH 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---LWLYGDEDY 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63 PFGKLC-----FHPASSVFHYGF---ECFEGMK---AFRDE------KG 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2; Length 380;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 4.4%; Score 88; DB 2; Length 380. Rest Local Similarity 19.6%; Pred. No. 9.9; Matches 67; Conservative 55; Mismatches 121; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Genome: nuclear
C;Superfamily: branched-chain-amino-acid transaminase BAT1
C;Keywords: aminotransferase; mitochondrion
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A;Gene: SPBC428.02c; SPBC582.12c
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A.Cross-references: UNIPROT: 0987L2; EMBL:AL035526
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

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5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
GenCore version 5.1.6
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                                                     EHRPLOKYMVWSDEMVKTGEAQIHAHLVRPYVGIHLRIGSDWKNACAMLKDGTAGSHFMA
                                       EGNPFGPFWDQFHVSFNKSELFTGISFSASYREQWSQRFSPKEHPVLALPGAPAQFPVLE
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Query Match

100.0%; Score 1979; DB 3; Length 3:

Best Local Similarity 100.0%; Pred. No. 2.4e-214;

Matches 365; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                          US-09-333-729A-3

US-09-333-729A-3

Sequence 3, Application US/09333729A

Petent No. 6270987

GENERAL INFORMATION:

APPLICANT: Spellman, Michael W.

TITLE OF INVENTION: O-Fucosyltransferase

TITLE OF INVENTION: O-Fucosyltransferase

CURRENT APPLICATION NUMBER: US/09/333,729A

CURRENT FILING DATE: 1999-06-15

PRIOR PELICATION NUMBER: US 08/798,741

PRIOR PLIANG DATE: 1997-11-26

NUMBER OF SEQ ID NOS: 21

LENGTH: 365

WOUNDER OF SEQ ID NOS: 21

LENGTH: 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
CORGANISM: Homo Sapien
US-09-333-729A-3
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121 EGNPFGPFWDQFHVSFNKSELFTGISFSASYREQWSQRFSPKEHPVLALPGAPAQFPVLE 180
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NESULT 3

US-08-978-741-6

Sequence 6, Application US/08978741

Sequence 6. 100076

Sequence 6. 100076

GENERAL INFORMATION:

APPLICANT Yang Wang, Michael W. Spellman TITLE OF INVENTION: 0-Fucosyltransferase NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS: 3

ADDRESSEE: Genentech, Inc.
STRET: 1 DNA Way

CITY: South San Francisco

STATE: California

COMPTER REDAble FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: BMP C compatible

COMPUTER: BMP C compatible

OPERATION SYSTEM PC-DOS/MS-DOS

SOFTWARE: MINPER: US/08/978,741

FILING DATE: 26-No. 610076-1997

CLASSIFICATION NUMBER: US/08/978,741

FILING DATE: 31

ATTORNEY/AGENT INFORMATION:

NAME: SVODOGA, Craig G.

REGISTRATION NUMBER: 39,044

REFERENCE/DOCKET NUMBER: 39,044

REGISTRATION NUMBER: 39,044

REGISTRATION NUMBER: 39,044

REGISTRATION NUMBER: 39,044

REGISTRATION NUMBER: 39,044

REGISTRATION NUMBER: 100: 6

REGISTRATION NUMBER: 100: 6

REGISTRATION NUMBER: 100: 6

SEQUENCE CHARACTERISTICS:

INFORMATION FOR SEG ID NO: 6

SEGUENCE CHARACTERISTICS:

INFORMATION FOR SEG ID NO: 6

SEGUENCE CHARACTERISTICS:

INFORMATION ADDITION:

TTELEPHONE: Amino Acid

TUPPE: Amino Acid
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Best Local Similarity 100.0%; Pred. No. 2.8e-214;
Matches 365; Conservative 0; Mismatches 0;
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OPERATING SYSTEM:
SOFTWARE: WinPati
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US-09-333-729A-13
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; Patent No. 6100076
; GENERAL INFORMATION:
    APPLICANT: Yang Wang, Michael W. Spellman
; TITLE OF INVENTION: O-Fucosyltransferase
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA WAY
CITY: South San Francisco
                                                                                                                            Sequence 7, Application US/0933729A
Patent No. 6270987
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Spellman, Michael W.
APPLICANT: Spellman, Michael W.
TITLE OF INVENTION: O-Fucosyltransferase
FILE REFERENCE: P1041P1D1-Substitute
CURRENT FILING DATE: 1999-06-15
PRIOR APPLICATION NUMBER: US/09/333,729A
CURRENT FILING DATE: 1997-11-26
NUMBER OF SEQ ID NOS: 21
LENGTH: 397
LENGTH: 397
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361 LRDEF 365
                                393 LRDEF 397
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143 TGISFSASYREQWSQRFSPKEHPVLALPCAPAOPPVLEEHRPLQKYMVWSDEMVKTGEAQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               203 IHAHLVRPYVGIHLRIGSDWKNACAMLKDGTAGSHFMASPQCVGYSRSTAAPLTMTMCLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23 NOADHFLGSLAFAKILNRTLAVPPWIEYQHHKPPFTNLHVSYQKYFKLEPLQAYHRVISL
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93.2%; Score 1844; DB 3; I
Best Local Similarity 100.0%; Pred. No. 3.8e-199;
Matches 343; Conservative 0; Mismatches 0;
                                      MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 13, Application US/0933729A
; Sequence 13, Application US/0933729A
; GENERAL INFORMATION:
; APPLICANT: Wang, Yang
; APPLICANT: Wang, Yang
; APPLICANT: Wang, Yang
; APPLICANT: BPELIANTION: O-FUCOSYLTANTEERE
; TILE REFERENCE: P1041P1D1-Substitute
; CURRENT APPLICATION NUMBER: US/09/333,729A
; CURRENT FILING DATE: 1999-06-15
; PRIOR PILING DATE: 1999-11-26
; NUMBER OF SEQ ID NOS: 21
; SEQ ID NO 13
; LENGTH: 343
                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,741
FILING DATE: 26-No. 6100076-1997
CLASSIFFCATION: 435
PRIOR APPLICATION NUMBER: 08/792498
FILING DATE: 31
ATTORNEY/AGENT INFORMATION:
NAME: SVODOGA, CARAGGG, REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: 99,044
                                                                                                                       WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 650/225-1489
TELEPAX: 650/922-9881
INPERMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 343 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inc
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79 VISLEDFMEKLAPTHWPPEKRVAYCFEVAAQRSPDKKTCPMKEGNPFGPFWDQFHVSFNK 138
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260 LFASPQCLGYKNERGA-LYPELCMPSKEAIIRQLKRTIKNVRQTQPDNEIKSVFVASDSN 318
                                                                                   291 SYVPELQ-QLFKGKVKVVSLKPEVAQVDLYILGQADHFIGNCVSSFTAFVKRERDLQGRP 349
                                                                                                                                    19 GRFGNOADHFLGSLAFAKLLNRTLAVPPWIEYQHHKPPFTNLHVSYQKYFKLEPLQAYHR
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27.4%; Score 541.5; DB 3; Length 474;
Best Local Similarity 36.2%; Pred. No. 5.6e-52;
Matches 125; Conservative 60; Mismatches 107; Indels 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Winheatin (Genentech) CURRENT APPLICATION NUMBER: US/08/978,741 FILING DATE: 26-NO. 6100076-1997 CLASSIFICATION NUMBER: 08/792498 PRIOR APPLICATION NUMBER: 08/792498 APPLICATION NUMBER: 08/792498 APPLICATION NUMBER: 31 FULNG DATE: 31 FULNG DATE: 31 FULNG DATE: 31 FULNG DATE: 31 FULNG DATE: 31 FULNG DATE: 31 FULNG DATE: 31 FULNG DATE: 31 FULNG DATE: 31 FULNG DATE: 31 FULNG DATE: 31 FULNG DATE: 31 FULNG DATE: 31 FULNG DATE: 31 FULNG DATE: 31 FULNG DATE: 31 FULNG DATE: 31 FULNG DATE: 31 FULNG DATE: 31 FULNG DATE: 31 FULNG DATE: 31 FULNG DATE: 31 FULNG DATE: 31 FULNG DATE: 31 FULNG DATE: 31 FULNG DATE: 31 FULNG DATE: 31 FULNG DATE: 31 FULNG DATE: 31 FULNG DATE: 31 FULNG DATE: 31 FULNG DATE: 31 FULNG DATE: 31 FULNG DATE: 31 FULNG DATE: 31 FULNG DATE: 31 FULNG DATE: 31 FULNG DATE: 31 FULNG DATE: 31 FULNG DATE: 31 FULNG DATE: 31 FULNG DATE: 31 FULNG DATE: 31 FULNG DATE: 31 FULNG DATE: 31 FULNG DATE: 31 FULNG DATE: 31 FULNG DATE: 31 FULNG DATE: 31 FULNG DATE: 31 FULNG DATE: 31 FULNG DATE: 31 FULNG DATE: 31 FULNG DATE: 31 FULNG DATE: 31 FULNG DATE: 31 FULNG DATE: 31 FULNG DATE: 31 FULNG DATE: 31 FULNG DATE: 31 FULNG DATE: 31 FULNG DATE: 31 FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULNG FULN
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CORRESPONDENCE ADDRESS:
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REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P1041P1
TELECOMMUNICATION INPORMATION:
TELEPRANE: 650/225-1489
TELEFRA: 650/952-9881
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 8
US-08-978-741-8
; Sequence 8, Application US/08978741
; Patent No. 6100076
; Patent INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Genentech, Inc. STREET: 1 DNA Way CITY: South San Francisco STATE: California
                                                                                                                                                                                                                                                     350 SSFFGMDRPPKLRD 363
                                                                                                                                                                                                                                                                                                                              379 SYFWGF---PKEKD 389
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TYPE: Amino Acid
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| Sequence 45921, Application US/09270767
| Patent No. 6703491
| CarberAL INFORMATION:
| APPLICANT: Homburger et al.
| TILE OF INVERNATION: Nucleic acids and proteins of Drosophila melanogaster:
| TILE REPRENENCE: File Reference: 7326-094
| CURRENT PPLICATION NUMBER: US/09/270,767
| CURRENT FILING DATE: 1999-03-17
| CURRENT FILING DATE: 1999-03-17
| SOFTWARE: PatentIN Ver. 2.0
| SEQ ID NO 45921
| LENGTH: 399
| TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TYPE: PRF | TY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 EDFMEKCLAPTHWPPEKRVAYCFEVAAQRSPDKKTCPWKEGNPFGPFWDQFHVSFNKSELF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 IHAHLVRPYVGIHLRIGSDWKNACAMLKDGTAGSHFMASPQCVGYSRSTAAPLTMTMCLP 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    142
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                                                                                                                                                                                                                                                                                                                                             83 EDFMEKLAPTHWPPEKRVAYCFEVAAQRSPDKKTCPMKEGNPFGPFWDQFHVSFNKSELF
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0
                                                                                                                                                                           Length 343;
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42.3%; Score 837; DB 4; Length 399;
Best Local Similarity 44.9%; Pred. No. 1.9e-85;
Matches 168; Conservative 62; Mismatches 118; Indels
                                                                                                                                                                                                                                                     0; Indels
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                                                                                                                                                                           Query Match 93.2%; Score 1844; DB 3; L
Best Local Similarity 110.0%; Pred. No. 3.8e-199;
Matches 343; Conservative 0; Mismatches 0;
         ; TYPE: PRT
; · ORGANISM: Homo Sapien
US-09-333-729A-13
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RESULT 12
US-09-270-767-61459
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     254 PLIMIMCLPDLKEIQRAVKLWVRSLDAQSVYVATDSESYVPELQQLFKGKVKVVSLKPEV 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              166 GRFGNQVDQFLGVLAFAKALDRTLVLPNFIEFKH---PETKM-IPFEFLFQVGTVAKYTR 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79 VISLEDFMEKLAPTHWPPEKRVAYCFEVAAQRSPDKKTCPMKEGNPFGPFWDQFHVSFNK 138
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----LEQ-----IEAHRQEPDD 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 27.4%; Score 541.5; DB 3; Length 474; Best Local Similarity 36.2%; Pred. No. 5.6e-52; Matches 125; Conservative 60; Mismatches 107; Indels 53.
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                                                                                  314 AQVDLYILGQADHFIGNCVSSFTAFVKRERDLQG---RPSSFFGM 355
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Fatent No. 6100076
GENERAL INFORMATION:
APPLICANT: Yang Wang, Michael W. Spellman ITILE OF INVENTION: O-Pucosyltransferase NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genettech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                        GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wang Yang
APPLICANT: Spellman, Michael W.
TITLE OF INVENTION: O'FUCOSYltransferase
CURRENT APPLICATION NUMBER: US/09/333,729A
CURRENT FILING DATE: 1999-06-15
PRIOR FILING DATE: 1997-11-26
NUMBER OF SEQ ID NOS: 21
SEQ ID NO 12
                                                                                                                                                                                                     Sequence 12, Application US/09333729A Patent No. 6270987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Caenorhabditis Elegans
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395 -LTKEICSPSKQQI--
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COMPUTER READABLE FORM:
                                                                                                                                                                    RESULT 9
US-09-333-729A-12
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1 MPAGSWDPAGYLLYCPCMGRFGNQADHFLGSLAFAKLLNRTLAVPPWIBYQHHKPPFTNL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.0%; Pred. No. 4e-32;
Matches 61; Conservative 0; Mismatches 0; Indels
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: 1BM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Winbatin (Genentech) CURRENT APPLICATION DATA: US/08/978,741 FILING DATE: 26-No. 6100076-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/0933729A
Patent No. 6270987
GENERAL INFORMATION:
APPLICANT: Wangy Yang
APPLICANT: Wangy Yang
TITLE OF INVENTION: O-Fucosyltransferase
FILE REFERENCE: P1041P1D1-Substitute
FILE REPERENCE: 19041P1D1-Substitute
CURRENT FILING DATE: 1999-06-15
PRIOR APPLICATION NUMBER: US/09/333,729A
CURRENT FILING DATE: 1997-11-26
NUMBER OF SEQ ID NOS: 21
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Prec. ... o; Mismatches
                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/792498
FILING DATE: 31
ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,04
REFRENCE/DOCKET NUMBER: P1041P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/952-9481
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CRASCTERISTICS:
LENGTH: 61 amino acids
TYPE: Amino Acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ropology: Linear
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Best Local Similarity
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US-09-333-729A-4
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us-09-774-954-2.rai

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, TYPE: Amino acids
; TOPOLGY: Linear
US-08-978-741-3
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                                                                                                                                                    Query Match
Best Local S
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117 DSNHHIGELNTALSKHKLTEDDPYLDLAILGQSNHFIGKOLTSSYSAFVKRERDH 176
117 DSNHHIGELNTALSKHKLTEDDPYLDLAILGQSNHFIGKOLTSSYSAFVKRERDH 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    176 FPVLEEHRPLQKYMVWSDEMVKTGEAQIHAHLVR-PYVGIHLRIGSDWKNACAMLKDGTA 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           235 GSHFMASPQCVGYSRSTAAPLTMTMCLPDLKEIQRAVKLWVRSL------DAQSVYVAT 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 61459, Application US/09270767
Patent No. 6703491
GENERAL INPORMATION:
APPLICANT: Homburger et al.
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REPERBNCE: File Reference: 7336-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 61459
LENGTH: 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                       16; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
17.3%; Score 343; DB 4; Length 200;
Best Local Similarity 40.6%; Pred. No. 3.5e-30;
Matches 80; Conservative 34; Mismatches 67; Indels
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ZIF: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Winheatin (Genentech)
SOFTWARE: Winheatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,741
FILING DATE: 26-NO. 610076-1997
CLASSIFICATION NUMBER: 08/792498
FILING DATE: 31
ATTORNEY/AGENT IRFORMATION:
MARME: SVOboda, Craig G
REGISTRATION NUMBER: 39,044
REGISTRATION NUMBER: P1041P1
TELECOMMUNICATION NUMBER: P1041P1
TELECOMMUNICATION NUMBER: P1041P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/08978741
Sequence 3, Application US/08978741
Sequence 3, Application US/08978741
Sequence 3, Application US/08978741
Sequence 3, Application US/08978741
Sequence 3, Application O-Fucesyltransferase NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS: ADDRESSE: Generatech, Inc.
STREET: 1 DNA May
CITY: South San Francisco
STARE: California
                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-61459
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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US-08-978-741-3
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                                                                                                                                         3 AGSWDLAGYLLYXPXMGRFGNQADHFLGSLAFAKLXVRTLAVPPWIEYQHHKPPFTNLH 61
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                                                          Gaps
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Best Local Similarity 91.5%; Pred. No. 1.4e-25;
Matches 54; Conservative 0; Mismatches 5; Indels
      Length 61;
ch 14.9%; Score 295; DB 3; Length 61 Similarity 91.5%; Pred. No. 1.4e-25; 54; Conservative 0; Mismatches 5; Indels
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech) SOFTWARE: WinPatin (Genentech) APPLICATION NUMBER: 08/08/978,741 FILING DATE: 26-NO. 6100076-1997 CLASSIPICATION 1435 PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/792498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Yang Wang, Michael W. Spellman TITLE OF INVENTION: O-Fucosyltransferase NUMBER OF SEQUENCES: 17 CORRESPONDENCE ADDRESS: ADDRESSE: Genemeted, Inc. STREET: 1 DNA WAY CITY: South San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Wang, Yang
APPLICANT: Spellman, Michael W.
APPLICANT: Spellman, Michael W.
TITLE OF INVENTION: O-FUCOSyltransferase
FILE REFERENCE: P1041P1D1-Substitute
CURRENT APPLICATION NUMBER: u5/99/333,729A
CURRENT FILING DATE: 1999-06-15
PRIOR APPLICATION WUMBER: US 08/798,741
PRIOR FILING DATE: 1997-11-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: unsure; LOCATION: 15, 17, 38
OTHER INFORMATION: unknown amino acid
US-09-333-729A-5
                                                                                                                                                                                                                                                           KESOUL 1.
18-09-333-729A-5
; Sequence 5, Application US/09333729A
; Patent No. 6270987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | 18-08-978-741-14 | Sequence 14, Application US/08978741 | Patent No. 6100076 | GENERAL INPORMATION: |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Cricetulus Grieseus
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| FILING DATE: 31
| ATTORNEY/AGENT INFORMATION:
| NAME: Svoboda, Craig G. |
| REGISTRATION NUMBER: 39.044 |
| REFERENCE/DOCKET NUMBER: P1041P1 |
| TELECOMUNICATION INFORMATION: |
| TELEFRAX: 650/225-1489 |
| INFORMATION FOR SEQ ID NO: 14: |
| SEQUENCE CHARACTERISTICS: |
| LENGTH: 28 amino acids |
| TYPE: Amino Acid |
| TOPOLGY: Linear |
| Couery Match |
| Best Local Similarity 90.0%; Pred: No. 0.00031; Matches 18; Conservative 0; Mismatches 2; Indels |
| Matches 18; Conservative 0; Mismatches 2; Indels |
| MPAGSWDPAGYLLYCPCMGR 20 |
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| Db 9 MPAGSWDPAGYLLYCPCMGR 28
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0; Gaps

Search completed: October 25, 2005, 15:42:47 Job time : 60.9589 secs

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Walika, M. 091774954 Page 1 Seg. 10s 2, 349

GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

October 25, 2005, 15:20:23 Run on:

, Search time 232.341 Seconds (without alignments) 607.588 Million cell updates/sec

1 MPAGSWDPAGYLLYCPCMGR......QGRPSSFFGMDRPPKLRDEF 365

US-09-774-954-2 1979 Title: Perfect score: Sequence:

2105692 seqs, 386760381 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Scoring table:

2105692 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A Geneseq 16Dec04:* 1: geneseqp1980s:* 2: geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp20048:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Aaw80571 Human hea	Abm82223 Tumour-as	Aaw80573 Human O-f	Aam78377 Human pro	-		Abb63790 Drosophil		Abg63619 Human alb	Adl76884 Albumin f	Aaw80574 N-termina	Aaw80572 N-termina	Abg95669 Human nuc	Abb69800 Drosophil	Ads96504 Drosophil	1 Human	ы		Aag55221 Arabidops	•	N	Aap94265 Sequence	N-term	Human	Abm84902 Human dia
SUMMARIES	ID	AAW80571	ABM82223	AAW80573	AAM78377	AAM79361	AAW80577	ABB63790	AAE03110	ABG63619	ADL76884	AAW80574	AAW80572	ABG95669	ABB69800	ADS96504	ABG95651	AAY87325	AAB40332	AAG55221	ABJ25654	AAG60442	AAP94265	AAW80575	ABM84900	ABM84902
	DB	5	8	~	4	4	~	4	4	ß	ω	~	~	'n	4	œ	ហ	ო	m	ო	ø	m	Н	N	œ	œ
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de	o to	100.0	100.0	100.0	94.4	93.8	93.2	42.0	40.9	40.9	40.9	17.8	14.9	8.3	8.1	8.1	7.2	6.1	5.3	. 5.3	5.2	5.2	5.1	5.1	5.1	5.1
	. ă	1979	1979	1979	1867.5	1855.5	1844	831	809	809	809	353	295	164.5	159.5	159.5	142	120	105.5	104	102.5	102	101.5	101	100.5	100.5
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ء بلو ټلو	Human H	Human Human	Abm84901 Human dia Adi95094 Novel NOV		Aab49313 Mouse bro	Abu35306 Protein e	Adl06054 M. catarr		Abu25276 Protein e	Abu45346 Protein e	Adb97786 Human alp	_	Abp73947 Candida a	Ade95586 Human NOV	Abg25040 Novel hum
ABM84903 ABM84899	ADE95590 ADE95588	AAB42097 ADA21127	ABM84901	ADC71275	AAB49313	ABU35306	ADL06054	AAY54319	ABU25276	ABU45346	ADB97786	ABG93234	ABP73947	ADE95586	ABG25040
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5.1	5.1	0. 4 0. 8.	4, 4	4.7	4.7	4.7	4.7	4.7	4.6	4.6	4.6	4.6	4.6	4.6	4.6
100.5	100	98.5 94.5	94.5	9.5	93	92.5	92.5	92.5	92	92	91.5	91	91	90.5	90.5
26	7 8 7 8 7 8	30	32	, E	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

1. .61 /note= "N-terminal sequence claimed for in claim 4" O-fucosyltransferase; epidermal growth factor; EGF; glycosylation; O-fucose; inhibitor; sensory neuron; retinal neuron; human; heart. Location/Qualifiers Ą. Human heart O-fucosyltransferase. AAW80571 standard; protein; 365 97US-00792498. 97US-00978741. 97WO-US023401 (first entry) Homo sapiens. 17-DEC-1997; 31-JAN-1997; 26-NOV-1997; WO9833924-A1 16-DEC-1998 06-AUG-1998. AAW80571; Key Peptide RESULT 1 AAW8057

(GETH) GENENTECH INC. Wang Y, Spellman MW;

WPI; 1998-437477/37. N-PSDB; AAV65632 Human O-fucosyl:transferase able to glycosylate epidermal growth factor domains - useful for diagnosis and treatment of diseases involving overexpression of the enzyme.

Example 1; Fig 12A; 90pp; English.

This represents a human heart O-fucosyltransferase that can glycosylate an epidermal growth factor (EGF) domain of a polypeptide with an activated O-fucose residue. Inhibitors of O-fucosyltransferase, e.g. mutants with increased affinity for the EFG domains, are used in diagnosis and treatment of conditions associated with overexpression of O-fucosyltransferase, to promote survival of sensory (retinal) neurons. Probes based on EGF domain polypeptide are used to detect gene

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RESULT 3
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                                                                                                                                          61 HVSYQKYFKLEPLQAYHRVISLEDFMEKLAPTHWPPEKRVAYCFEVAAQRSPDKKTCFWK 120
                                                                                                                                                                    180
                                                                                                                                                                              SPOCYGYSRSTAAPLTMTMCLPDLKEIQRAVKLWVRSLDAQSVYVATDSESYVPELQQLF 300
                                                                                                                                                                                                                                                                                          KGKVKVVSLKPEVAQVDLYILGQADHFIGNCVSSFTAFVKRERDLQGRPSSFFGMDRPPK 360
                                                                                                                             HVSYQKYFKLEPLQAYHRVISLEDFMEKLAPTHWPPEKRVAYCFEVAAQRSPDKKTCPMK 120
                                                                                       9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tumour-associated antigenic target (TAT) polypeptide PRO83146, SEQ:5726
amplification and expression. The expression can also be determined at the protein level using antibodies specific for O-fucosyltransferase
                                                                                                                                                                     EGNPFGPFWDQFHVSFNKSELFTGISFSASYREQWSQRFSPKEHPVLALPGAPAQFPVLE
                                                                                                                                                                                                             EHRPLOKYMVWSDEMVKTGEAQIHAHLVRPYVGIHLRIGSDWKNACAMLKDGTAGSHFMA
                                                                                                          1 MPAGSWDPAGYLLYCPCMGRFGNQADHFLGSLAFAKLLNRTLAVPPWIEYQHHKPPFTNL
                                                                                       1 MPAGSWDPAGYLLYCPCMGRFGNQADHFLGSLAFAKLLNRTLAVPPWIBYQHHKPPFTNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tumour-associated antigenic target; TAT; human; overexpression; catumour; diagnosis, cell proliferative disorder; breast cancer; colorectal cancer; lung cancer; lung cancer; lung cancer; lung cancer; central nervous system cancer; bladder cancer; pancreatic cancer; certical cancer; melanoma; leuvésemia; hybridisation probe; chromosome identification; chromosome mapping; gene mapping;
                                                                    ..
                                                Length 365
                                                                  0; Indels
                                                ; Score 1979; DB 2;
; Pred. No. 2.5e-205;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                       ABM82223 standard; protein; 388 AA.
                                                Query Match
100.0%;
Sest Local Similarity 100.0%;
Matches 365; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-OCT-2002; 2002US-0414971P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-SEP-2003; 2003WO-US028547
                                                                                                                                                                                                                                                                                                                                                                                                                                             18-NOV-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zhang Z, Zhou Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene therapy; cytostatic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2004-347921/32.
N-PSDB; ACN40746.
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                              Sequence 365 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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The invention relates to human tumour-associated antigenic target (TAT) polypeptides, and their related nucleic acids. The TAT polypeptides are oversxpressed in cancer tissues compared to normal tissues, and may thus convexpressed in cancer tissues compared to normal tissues, and may thus serve as effective targets for the diagnosis and treatment of cancer in mammals. The invention also relates to nucleic acid and polypeptide of sequences at least 80% identical to the TAT mucleic acids and complexition and polypeptides, expression vectors and host cells comprising and mit body specific for a TAT polypeptide; fusion proteins comprising a confidence in mammals. TAT polypeptides, motering comprising and proceed in mammals. TAT polypeptides, mucleic acids, antipodies, antagonists, binding molecules and compositions are useful antipodies, antagonists, binding molecules and compositions are useful concersed that expression, particularly cancers such as breast cancer, increased TAT expression, particularly cancers such as breast cancer, cancer, panceatic cancer, lung cancer, oavarian cancer, liver cancer, bladder cancer, lung cancer, oavarian cancer, cancer of the central cancer, lung cancer, oavarian cancer, cancer of the central cancer, bancatic cancer, cervical cancer, cancer such any further be curved as hybridisation probes, in chromosome and gene mapping, in chromosome identification and in gene therapy. The present sequence the cancer and the cancer and compared the cancer and cancer and cancer and compared and cancer and cancer and cancer and cancer and cancer and cancer and cancer and cancer and cancer and cancer and cancer and cancer and cancer and cancer and cancer and cancer and cancer and cancer and cancer and cancer and cancer and cancer and cancer and cancer and cancer and cancer and cancer and cancer and cancer and cancer and cancer and cancer and cancer and cancer and cancer and cancer and cancer and cancer and cancer and cancer and cancer and cancer and cancer and cancer and cancer and cancer and can
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             143
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New tumor-associated antigenic target polypeptides and nucleic acids, useful in preparing a medicament for treating or detecting a proliferative disorder, e.g. breast, lung, colorectal, ovarian or prostate cancer or tumor.
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100.0%; Score 1979; DB 8;
Best Local Similarity 100.0%; Pred. No. 2.7e-205;
Matches 365; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                          Claim 12; SEQ ID NO 5726; 7273pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 388 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-DEC-1998
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7 DPAGYLLYCPCM-----GRFGNQADHFLGSLAFAKLLNRTLAVPPWIEYQHHKPPFTNLH 61
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                                                                                                                                                                                                                                                                                                                                                        27-APR-2000; 2000US-00560875.
20-JUN-2000; 2000US-00598075.
19-JUL-2000; 2000US-00620325.
                                                                                                                                                                                                                                                                                                                                                                                            01-SEP-2000; 2000US-00654936.
15-SEP-2000; 2000US-00653561.
20-OCT-2000; 2000US-00693325.
30-NOV-2000; 2000US-00728422.
                                                                                                                                                               Human protein SEQ ID NO 1039.
                                                                                                                                                                                                                                                                                                                      05-FEB-2001; 2001WO-US004098
                                                                                                                                                                                                                                                                                                                                              03-FEB-2000; 2000US-00496914.
                                                                                                                                        06-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wang D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 350; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tang YT, Liu C,
Ma Y, Zhao QA, Wa
Y, Yang Y, W
           LRDEF 365
                                 LRDEF 397
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                                                                                                                                                                                                                                                                        WO200157190-A2
                                                                                                                                                                                                                                                  Homo sapiens
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           361
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                                                                                                                  AAM78377;
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Best Local &
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                                                                                                                                                                                                                                                                                                                                                                                                                 domain of a polypeptide with an activated O-fucose residue. Inhibitors of O-fucosyltransferase, e.g. mutants with increased affinity for the EFG domains, are used in diagnosis and treatment of conditions associated with overexpression of O-fucosyltransferase, to promote survival of sensory (retinal) neurons. Probes based on EGF domain polypeptide are used to detect gene amplification and expression. The expression can also be determined at the protein level using antibodies specific for O-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KGKVKVVSLKPEVAQVDLYILGQADHFIGNCVSSFTAFVKRERDLQGRPSSFFGMDRPPK 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HVSYQKYPKLEPLQAYHRVISLEDFMEKLAPTHWPPEKRVAYCPEVAAQRSPDKKTCPMK 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPQCVGYSRSTAAPLTMTMCLPDLKEIQRAVKLWVRSLDAQSVYVATDSESYVPELQQLF 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92
                                                                                                                                                                                                                                                                                                           Human O-fucosyl:transferase able to glycosylate epidermal growth factor domains - useful for diagnosis and treatment of diseases involving
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MPAGSWDPAGYLLYCPCMGRFGNQADHFLGSLAFAKLLNRTLAVPPWIEYQHHKPPFTNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HVSYQKYFKLEPLQAYHRVISLEDFMEKLAPTHWPPEKRVAYCFEVAAQRSPDKKTCPMK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                 This represents the amino acid sequence of the human heart O-fucosyltransferase expressed by a plasmid insertion. The human O-fucosyltransferase can glycosylate an epidermal growth factor (EGF)
O-fucosyltransferase; epidermal growth factor; EGF; glycosylation;
O-fucose; inhibitor; sensory neuron; retinal neuron; human; heart.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 1979; DB 2;
llarity 100.0%; Pred. No. 2.8e-205;
Conservative 0; Mismatches 0;
                                                                                          /note= "polyhistidine tag"
                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                             Example; Fig 13B; 90pp; English
                                                                                                                                                                                                                                                                                                                                    overexpression of the enzyme.
                                                                                                                                                                                         97US-00792498.
                                                                                                                                                                  97WO-US023401
                                                                                                                                                                                                                           GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                   Wang Y, Spellman MW;
                                                                                                                                                                                                                                                                         WPI; 1998-437477/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
es 365; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eucosyltransferase
                                                                                                                                                                                                                                                                                       N-PSDB; AAV65633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 397 AA;
                                                                                                                                                                                          31-JAN-1997;
                                                                                                                                                                                                      26-NOV-1997;
                                     sapiens
                                                                                                                                                                  17-DEC-1997;
                                                                                                                    WO9833924-A1
                                                                                                                                            06-AUG-1998
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Best Local Si
Matches 365
                                                 Synthetic
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                                                                                Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce
                                                                                                                                                                                                                                                                                         Human, cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
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Wang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xu C, Cao
Chen R,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drmanac RT, Asundi V, Zhou P, Xt
Nang D, Wang J, Zhang J, Ren F,
Wejhrman T, Goodrich R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94.4%; Score 1867.5; DB 4 96.2%; Pred. No. 3.8e-193;
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AAM78377 standard; protein; 417 AA.
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Homo sapiens
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26-NOV-1997;
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                                                          Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy.
                                         173
                                                                                                    PQCVGYSRSTAAPLIMIMCLPDLKEIQRAVKLWVRSLDAQSVYVATDSBSYVPELQQLFK 353
54 DMATWPTHAPSVEEGGGGRFGNQADHFLGSLAFAKLINRTLAVPPWIEYQHKPPFTNLH 113
                          121
                                                                                          HRPLOKYMVWSDEMVKTGEAQIHAHLVRPYVGIHLRIGSDWKNACAMLKDGTAGSHFWAS 241
                                                                                                                          PQCVGYSRSTAAPLIMIMCLPDLKEIQRAVKLWVRSLDAQSVYVAIDSESYVPELQQLFK 301
                                                                                                                                                                                                                                                                                                                  Human, cytokine; cell proliferation, cell differentiation, gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cao Y;
R, Wang ZW;
                          VSYOKYFKLEPLOAYHRVISLEDFMEKLAPTHWPPEKRVAYCFEVAAORSPDKKTCPMKE
                                    Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C,
Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen
Xue AJ, Yang Y, Wejhrman T, Goodrich R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 20; Page 229-230; 6221pp; English
                                                                                                                                                                                                                                                      AAM79361 standard; protein; 417 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                             03-FEB-2000; 2000US-00496914.
27-AFR-2000; 2000US-00560875.
20-UUN-2000; 2000US-00598075.
19-UUJ-2000; 2000US-0063032.
15-SEP-2000; 2000US-0065351.
20-CCT-2000; 2000US-0063325.
30-NOV-2000; 2000US-0063325.
                                                                                                                                                                                                                                                                                                                                                                                                               05-FEB-2001; 2001WO-US004098.
                                                                                                                                                                                                                                                                                                     Human protein SEQ ID NO 3007
                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HYSE-) HYSEQ INC.
                                                                                                                                                                                             RDEF 365
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                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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                                                                                                                                            294
                                                                                                                            242
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                                                                                                                                                                                                                                                                      AAM79361;
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The invention relates to polymuclectides (AAK51456-AAK53435) and the encoded polypeptides (AAW78323-AAM89302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polymptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides are useful in gene therapy, vaccines or e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity, tissue growth factor activity, immunomodulatory activity and activity indual may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122 GNPFGPFWDQFHVSFNKSELFTGISFSASYREQWSQRFSPKEHPVLALPGAPAQFPVLEE 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       182 HRPLOKYMVWSDEMVKTGEAQIHAHLVRPYVGIHLRIGSDWKNACAMLKDGTAGSHFMAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 DPAGYLLYCPCM-----GRFGNQADHFLGSLAFAKLLNRTLAVPPWIEYQHHKPPFTNLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 VSYQKYFKLIEPLQAYHRVISLEDFMEKLAPTHWPPEKRVAYCFEVAAQRSPDKKTCPMKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  O-fucosyltransferase; epidermal growth factor; EGF; glycosylation; O-fucose; inhibitor; sensory neuron; retinal neuron; human; heart.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
93.8%; Score 1855.5; DB 4; Length 417;
Best Local Similarity 95.6%; Pred. No. 7.6e-192;
Matches 348; Conservative 4; Mismatches 7; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW80577 standard; protein; 343 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97US-00792498.
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67 YFKLEPLQAYHRVISLEDFMEKLAPTHWPPEKRVAYCFE----VAAQRSPDKKTCPMKE 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HHIGELNTALSRMGISVHKLPEDDPYLDLAILGQSNHFIGNCISSYSAFEKRERDVHGFP 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   263 LFASPQCLGYKNERGA-LYPELCMPSKEAIIRQLKRTIKNVRQTQPDNEIKSVFVASDSN 321
                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA ABB72072). The sequence data for this parent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28 DPNGYLTYCPCMGRFGNQADHFLGSLAFAKALNRTLILPPWVEXR--RGELRSRQVPFNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122 GNPFGPFWDOFHVSFNKSELFTGISFSASYREQ---WSQRFSPKEHPVLALPGAPAQFPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       179 LEEHRPLQKYMVWSDEMVKTGEAQIHAHLVR-PYVGIHLRIGSDWKNACAMLKDGTAGSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              238 FMASPOCVGYSRSTAAPLTWTWCLPDLKEIQRAVKLWVRSL-----DAQSVYVATDSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 DPAGYLLYCPCMGRFGNQADHFLGSLAFAKLINRTLAVPPWIEYQHHKPPFTNLHVSYQK
                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 18162; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42.0%; Score 831; DB 4; Length 40
44.7%; Pred. No. 1.1e-80;
tive 62; Mismatches 119; Indels
                                                                                                                                                                                                    Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAE03110 standard; protein; 165 AA.
                                                                                                                                                                                                  Li PWD,
                                                     23-MAR-2001; 2001WO-US009231.
                                                                                             23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 44.7
Matches 167; Conservative
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                                                                                                                                                                                                                                          WPI; 2001-656860/75
                                                                                                                                                           (PEKE ) PE CORP NY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 402 AA;
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                   27-SEP-2001
                                                                                                                                                                                                    Venter JC,
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Best Local 8
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                                                                                                                                                                                                                                                                             This represents a published partial human sequence of unknown function from a myeblast cell line. The invention provides a human heart Ofucosyltransferase enzyme that can glycosylate an epidermal growth factor (EGF) domain of a polypeptide with an activated Ofucose residue. Inhibitors of Ofucosyltransferase, e.g. mutants with increased affinity for the BFG domains, are used in diagnosis and treatment of conditions associated with overexpression of Ofucosyltransferase, to promote polypeptide are used to detect gene amplification and expression. The expression can also be determined at the protein level using antibodies specific for Ofucosyltransferase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                              Human O-fucosyl:transferase able to glycosylate epidermal growth factor domains - useful for diagnosis and treatment of diseases involving
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGISFSASYREQWSQRFSPKEHPVLALPGAPAQFPVLEEHRPLQKYMVWSDEMVKTGEAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IHAHLVRPYVGIHLRIGSDWKNACAMLKDGTAGSHFMASPQCVGYSRSTAAPLTMTMCLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EDFMEKLAPTHWPPEKRVAYCFEVAAQRSPDKKTCPMKEGNPFGPFWDQFHVSFNKSELF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23 NQADHFLGSLAFAKLLNRTLAVPPWIEYQHHKPPFTNLHVSYQKYFKLEPLQAYHRVISL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
93.2%; Score 1844; DB 2; Length 343;
Best Local Similarity 100.0%; Pred. No. 1e-190;
Matches 343; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        343
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                                                                                                                                                                                                                                               Example 1; Page 62-68; 90pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABB63790 standard; protein; 402 AA
                                                                                                                                                                                                        overexpression of the enzyme.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster.
                       (GETH ) GENENTECH INC
                                                           Wang Y, Spellman MW,
                                                                                                      1998-437477/37
                                                                                                                         N-PSDB; AAV65634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 343 AA;
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RESULT 7

82

Gaps

56;

Length 402;

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us-09-774-954-2.rag

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AAD07571-AAD07645 represent cDNAs corresponding to 25 human secreted protein genes, and AAE03122 represent the proteins they encode. AAE03127-AAE03150 represent the proteins they encode. AAE03127-AAE03150 represent human secreted protein fragments. The genes and their corresponding secreted proteins are useful for preventing, creating or amellorating medical conditions, e.g., by protein or gene therapy. Pathological conditions can be diagnosed by determining the camount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the and include developing products for the diagnosis or treatment of the and include developing products for the diagnosis or treatment of proliferative disorders, cancer, tumours, foetal and developmental abnormalities, haematopoietic disorders, diseases of the immune system, Calbergies, neurological disorders (e.g., Alzheiner's disease, allergies, neurological disorders (e.g., Alzheiner's disease, Parkinsons's disease), cognitive disorders, schizophrenia, asthma, skin
                                                                     Human, secreted protein, proliferative disorder; cancer; tumour; foetal abnormality; developmental abnormality; haematopoietic disorder; immune system disorder; ALDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; Alzheimer's disease; Parkinson's disease; cognitive disorder; schizophrenia; asthma; exim disorder; psortiasis; sepais; diabetes; atherosclerosis; cardiovascular disorder; angiogenic disorder; kidney disorder; gastrointestinal disorder; programoy-related disorder; gene endocrine disorder; infection; wound healing; vulnerary; cell culture; chemotaxis; food additive; chromosome 3; binding partner identification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acids encoding 25 human secreted polypeptides, useful for preventing, diagnosing and/or treating e.g. Gaucher's disease, Alzaheimer's disease, Scimitar syndrome, Creutzfeldt-Jacob disease, diabetes mellitus and multiple sclerosis.
                                      Human gene 18 encoded secreted protein HMWEY26, SEQ ID NO:144.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ruben SM, Komatsoulis GA, Shi Y, Olsen HS, Soppet DR;
                                                                                                                                                                                                                                                                                                                                                                                                                   "Mature secreted protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         'label= Unknown
'note= "Encoded by ANA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= Unknown
/note= "Encoded by NCA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note= "Encoded by TGA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= Unknown
/note= "Encoded by AGS"
                                                                                                                                                                                                                                                                                                                                                                    1. .1
/label= Signal_peptide
2. .165
/note= "Mature secreted
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                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            label= Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-OCT-2000; 2000WO-US029365.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-OCT-1999; 99US-0162237P.
21-JUL-2000; 2000US-0219666P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HUMA-) HUMAN GENOME SCI INC.
10-AUG-2001 (first entry)
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                                                                                                                                                                                                                                                                                                     Homo sapiens
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                                                                                                                                                                                                                                                                                                                                         Key
Peptide
                                                                                                                                                                                                                                                                                                                                                                                                 Protein
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disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders, angiogenic disorders, fidney disorders, gastrointestinal disorders, pregnancy-related disorders, endocrine disorders, and infections. The proteins can also be used to aid wound carding and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues, to identify their cognate ligands or binding partners, and in chemctaxis, and can be used as a food additive or preservative to modify storage properties.

Antibodies specific for a procein of the invention can be used in diagnostic immunosasys e.g., radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The present sequence represents a human in secreted protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                              206 HLVRPYVGIHLRIGSDWKNACAMLKDGTAGSHFMASPQCVGYSRSTAAPLTMTMCLPDLK 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66 BIQRAVKLWVRSLDAQSVYVATDSBSYVPELQQLFKGKVKVVSLKPEVAQVDLYILGQAD 125
                                                                                                                                                                                                                                                                                                                                                                                                                               65
                                                                                                                                                                                                                                                                                                                                                                                                                     EIORAVKLWVRSLDAQSVYVATDSESYVPELQQLFKGKVKVVSLKPEVAQVDLYILGQAD
                                                                                                                                                                                                                                                                                                                                                           0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Albumin fusion protein; therapeutic protein X; human albumin; HA; human serum albumin; HSA; cancer; reproductive disorder; digestive disorder; immune disorder; endocrine disorder; hematopoletic disorder; neural disorder; connective disorder; cytostatic; antiinfertility; antiinflammatory; antiulcer; immunomodulator; anti-HV, antidiabetic; haemostatic; nootropic; neuroprotective; antiparkinsonian; antimicrobial; neuroleptic; osteopathic; antiarthritic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New fusion protein for treating disease e.g. diabetes comprises
                                                                                                                                                                                                                                                                                                                     Length 165;
                                                                                                                                                                                                                                                                                                                   Query Match 40.9%; Score 809; DB 4; Length 16:
Best Local Similarity 96.9%; Pred. No. 6.6e-79;
Matches 155; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  126 HFIGNCVSSFTAFVKRERDLQGXPSSFFGMDRPPKLRDEF 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HFIGNCVSSFTAFVKRERDLQGRPSSFFGMDRPPKLRDEF 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABG63619 standard; protein; 165 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human albumin fusion protein #294.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-APR-2000; 2000US-0229358P.
25-APR-2000; 2000US-0199384P.
21-DEC-2000; 2000US-0256931P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-APR-2001; 2001WO-US011988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                    Sequence 165 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200177137-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       566
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
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The present invention relates to albumin fusion proteins comprising a therapeutic protein X and human albumin (HA, also known as human serum albumin, HSA). The proteins are useful for treating a disease or disorder that may be modulated by therapeutic protein X. The albumin extends the shelf-life of protein X, and may increase its biological in vitro/in vivo activity. The protein is useful for treating and diagnosing disorders activity. The protein is useful for treating and diagnosing disorders disease, ulcerative colitis), immune disorders (e.g. acquired immunodeficiency syndrome, AIDS), endocrine disorders (e.g. diabetes), hemancopoietic disorders, neural disorders (e.g. Alzheimer's, Parkinson's, Creutzfeldt-Jacob disease, encephalomyelitis, meningitis, schizophrenia), and connective disorders (e.g. osteoporosis, arthritis). ABG63326-ABG65518 represent albumin fusion proteins of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      albumin fusion protein; cytostatic; antianaemic; antiarthritic; antiasthmatic; anti-HIV; immunosuppressive; antiinflammatory; antipsoriatic; antibacterial; osteopathic; dermatological; antigout; immunomodulator; antiarrhythmic; cardiant; nootropic; antilipaemic; nephrotropic; uropathic; neuroprotective; antiparkinsonian; tranquilizer; antidiabetic; anabolic; hypertensive; vulnerary; gene therapy; cancer; reproductive system disorder; therapeutic protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            266 BIQRAVKLWVRSLDAQSVYVATDSESYVPELQQLFKGKVKVVSLKPEVAQVDLYILGQAD 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66 BIQRAVKLWVRSLDAQSVYVATDSESYVPELQQLFKGKVKVVSLKPEVAQVDLYILGQAD 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          206 HLVRPYVGIHLRIGSDWKNACAMLKDGTAGSHFMASPQCVGYSRSTAAPLTMTMCLPDLK 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 HFARTYPGIHLRIGSDWKNACAMLKDGTAGSHFWASPQCVGYSRSTAAPLTMTMCLPDLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Albumin fusion protein related therapeutic protein X, SEQ ID No 366.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               126 HFIGNCVSSFTAFVKRERDLQGXPSSFFGMDRPPKLRDEF 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   326 HFIGNCVSSFTAFVKRERDLQGRPSSFFGMDRPPKLRDEF 365
                                                                                                                                                                                                                                                                                                                                                                                                                         40.9%; Score 809; DB 5; Le 96.9%; Pred. No. 6.6e-79; iive 0; Mismatches 5;
albumin fused to a therapeutic protein.
                                     Claim 1; Page 755-756; 2102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADL76884 standard; protein; 165 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-APR-2000; 2000US-0229358P.
25-APR-2000; 2000US-0199384P.
21-DEC-2000; 2000US-0256931P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-APR-2001; 2001US-00833245.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-MAY-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 155; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rosen CA, Haseltine WA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ROSE/) ROSEN C A. (HASE/) HASELTINE W A.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2004-090519/09
                                                                                                                                                                                                                                                                                                                                                                                   Sequence 165 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unidentified
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                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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, treating, prevent anemia, arthritis, New albumin fusion proteins, useful for diagnosing, treatior ameliorating diseases or disorders e.g. cancer, anemia. asthma, inflammatory bowel disease or Alzheimer's disease.

Disclosure; SEQ ID NO 366; 279pp; English

c. The invention relates to a nowel albumin fusion protein no further relates to: a composition comprising the albumin fusion protein and a pharmaceutical carrier; a kit comprising the albumin fusion protein and a pharmaceutical carrier; a kit comprising the ambumin fusion protein a method of treating a patient with a disease or disorder that is modulated by Therapeutic protein: X, or its fragment or variant; a method of treating a patient with a disease or disorder that is modulated by Therapeutic protein: A or its fragment or variant; a method of extending the shall life of Therapeutic protein: X or its fragment or variant; a method of the albumin fusion protein; and a host cell or method of extending the albumin fusion protein; and a host cell or motieic acid molecule of the albumin fusion protein. The and its compositions have the following comprising the and its compositions have the following cultivatives: cytostatic, antihalmanent, antiporiatic, antihacterial, steppositic, dermatological antification; manupoupprosestive, antihalmanent, antihalmanent, antiporiatic, antihacterial, steppositic, dermatological antigon, transing protein moleic card may be used in gene therapy to treat disorders. The albumin fusion protein mucieic acid may be used in gene therapy to treat disorders. The albumin fusion protein cultured in disorders comprising indication; bone, breast, liver or lung cancer), immune of hematopoietic diseases (e.g. anaemia, Hodgkin's disease or disorders include:

C cancer (e.g. leuksemia, colon, bone, breast, liver or lung cancer of useful for disponsing, treating, preventing or ameliorating disease or disorders muciein disease, parameter, antipore meaning, multiple myelom, arthritis, stehm, Albian, autoimmune disease, protein disease, or disorders include disease, system disease (e.g. anaemia, Hodgkin's disease or disorders in multiple myelom, arthritis, stehm, Albian, autoimmune disease, parameter, proponetrial disease, system diseases (e.g. giant cell tumours) and disease, parameter, protein d invention relates to a novel albumin fusion protein.

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Gaps

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Length 165; Indels 9

Sequence 165 AA;

206 HLVRPYVGIHLRIGSDWKNACAMLKDGTAGSHFWASPQCVGYSRSTAAPLITWTMCLPDLK 265 6 HFARTYPGIHLRIGSDWRNACAMLKDGTAGSHFMASPQCVGYSRSTAAPLTWTWCLPDLK 65 40.9%; Score 809; DB 8; Length 165; 96.9%; Pred. No. 6.6e-79; 0; Mismatches Query Match Best Local Similarity 96.9 Matches 155; Conservative ္ခရ ઠે

266 BIQRAVKLWVRSLDAQSVYVATDSESYVPBLQQLFKGKVKVVSLKPEVAQVDLYILGQAD 325

66 EIQRAVKLWVRSLDAQSVYVATDSESYVPELQQLFKGKVKVVSLKPEVAQVDLYILGQAD 125

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326 HFIGNCVSSFTAFVKRERDLQGRPSSFFGMDRPPKLRDEF 365

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RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This represents a the N-terminal sequence of the human heart O-fucosyltransferase that can glycosylate an epidermal growth factor (EGF) domain of a polypeptide with an activated O-fucose residue. Inhibitors of O-fucosyltransferase, e.g. mutants with increased affinity for the EFG domains, are used in diagnosis and treatment of conditions associated with overexpression of O-fucosyltransferase, to promote survival of sensory (retinal) neurons. Probes based on EGF domain polypeptide are used to detect gene amplification and expression. The expression can also be determined at the protein level using antibodies specific for O-fucosyltransferase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MPAGSWDPAGYLLYCPCMGRFGNQADHFLGSLAFAKLLNRTLAVPPWIEYQHHKPPFTNL 60
                                                                                                                                                                                                                                                                                                                  Human O-fucosyl:transferase able to glycosylate epidermal growth factor domains - useful for diagnosis and treatment of diseases involving overexpression of the enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MPAGSWDPAGYLLYCPCMGRFGNQADHFLGSLAFAKLLNRTLAVPPWIEYQHHKPPFTNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                         N-terminal amino acid sequence of human heart O-fucosyltransferase.
                                                                                                            O-fucosyltransferase, epidermal growth factor; EGF; glycosylation;
O-fucose; inhibitor; sensory neuron; retinal neuron; human; heart.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-terminal amino acid sequence of CHO O-fucosyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 17.8%; Score 353; DB 2; Length 61 Best Local Similarity 100.0%; Pred. No. 4.4e-30; Matches 61; Conservative 0; Mismatches 0; Indels
                            AAW80574 standard; peptide; 61 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW80572 standard; peptide; 61 AA
                                                                                                                                                                                                                                                                                                                                                             Claim 4; Page 69; 90pp; English.
                                                                                                                                                                                                                          97US-00792498.
                                                                                                                                                                                                        97WO-US023401
                                                                     16-DEC-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                         (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                            Spellman MW;
                                                                                                                                                                                                                                                                                                WPI; 1998-437477/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fucosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 61 AA;
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26-NOV-1997;
                                                                                                                                           Homo sapiens
                                                                                                                                                               WO9833924-A1
                                                                                                                                                                                   06-AUG-1998
                                                  AAW80574;
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                                                                                                                                                                                                                                                                            Wang Y,
         RESULT 11
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AAW8057
                     AAW8057
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This represents the N-terminal sequence of CHO O-fucosyltransferase. The enzyme can glycosylate an epidermal growth factor (EGF) domain of a polypeptide with an activated O-fucose residue. Inhibitors of O-fucosyltransferase, e.g. mutants with increased affinity for the EFG domains, are used in diagnosis and treatment of conditions associated with overexpression of O-fucosyltransferase, to promote survival of sensory (retinal) neurons. Probes based on EGF domain polypeptide are used to detect game amplification and expression. The expression can also be determined at the protein level using antibodies specific for O-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human O-fucosyl:transferase able to glycosylate epidermal growth factor domains - useful for diagnosis and treatment of diseases involving voverexpression of the enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 AGSWDPAGYLLYCPCMGRFGNQADHFLGSLAFAKLLNRTLAVPPWIEYQHHKPPFTNLH 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 AGSWDLAGYLLYXPXMGRFGNQADHFLGSLAFAKLXVRTLAVPFWIEYQHHKPPFTNLH 61
O-fucosyltransferase; epidermal growth factor; EGF; glycosylation; O-fucose; inhibitor; sensory neuron; retinal neuron; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human nucleic acid associated protein, NAAP26, Incyte 7503717CD1.
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Pred. No. 8.6e-24;
0; Mismatches 5; Indels
                                                                                                                                                                 Location/Qualifiers
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                                                                                                                                                                                                                                    note= "unknown"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97WO-US023401
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Best Local Similarity 91.5%;
Matches 54; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GETH ) GENENTECH INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1998-437477/37.
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                                                                                                                                                                                                                                                                                                                                           Misc-difference 38
                                                                                                                                                                                                                                                                        Misc-difference 17
                                                                                                                                                                         Key
Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 61 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-JAN-1997;
26-NOV-1997;
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New human nucleic acid-associated proteins and polynucleotides, useful for diagnosing, treating or preventing cardiovascular, neurological, autoimmune or inflammatory disorders, e.g. atherosclerosis, Alzheimer's
                                                                                                                                                                                              Hillman JL, Baughn MR, Swarnakar A, Yue H, Elliott VS, Bu
Ding L, Tang YT, Lee SY, Azimzai Y, Walia NK, Gietzen KJ;
Grifffin JJ, Lal PG, Yang J, Borowsky ML, Richardson TW, Y
Becha S, Forsythe IJ, Jones KA, Warren BA, Thangavelu K;
Honchell CD, Jolley HE, Hafalia AJA, Ring HZ;
                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 193-194; 219pp; English.
Crohn's disease; multiple sclerosis.
                                                                                         2001US-0276857P.
2001US-0285489P.
2001US-028556F.
2001US-0288646P.
2001US-0288700P.
                                                                                                                                                    11-MAY-2001; 2001US-0290369P.
16-NOV-2001; 2001US-0332426P.
                                                                       14-MAR-2002; 2002WO-US007869
                                                                                                                                                                               (INCY-) INCYTE GENOMICS INC.
                                                                                                                                                                                                                                                           WPI; 2002-723448/78.
                                                                                                                                                                                                                                                                     N-PSDB; ABS73886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 328 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       an NAAP protein
                                    WO200274913-A2
                  Homo sapiens.
                                                                                                                        34-MAY-2001;
                                                                                                                                04-MAY-2001;
                                                                                                              19-APR-2001;
                                                                                                                                          10-MAY-2001;
                                                      26-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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Burford N;

Yue H;

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The invention relates to an isolated human nucleic acid-associated protein (NAAP), comprising the protein sequences appearing as ABG95644-CC protein (NAAP), comprising the protein sequences appearing as ABG95644-CC protein immunogenic or biologically active fragment. Also included are the NAAP encoding polynucleotides, a recombinant NAAP polynucleotide, a call transformed with the recombinant NAAP antibody, correning compounds as modulators or ant/agonists of NAAP antibody, correning compounds as modulators or ant/agonists of NAAP antibody, correning compounds as modulators or ant/agonists of NAAP or modulators or nucleotides of the NAAP polynucleotides and generating an expression profile of a sample that contains NAAP polynucleotides and generating an disease or condition associated with decreased expression of functional NAAP. The antagonist is useful for treating a disease or condition associated with the expression of functional NAAP. The antibody that specifically binds to the polypeptide is useful for diagnosing a condition or disease to the polypeptide is useful for diagnosing a condition or disease corrected with the expression of NAAP. These diseases include the polypeptide is useful for diagnosing a condition or disease or inflammatory disorders. These polypeptides, polynucleotides, agonists and antagonists may also be used for preventing these diseases. These and antagonists may also be used for preventing these diseases. These conditions associated with circle of the proventing these diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             syndrome (AIDS), Creutzfeldt-Jakob disease, Goodpasture's syndrome, Crohn's disease, or multiple sclerosis and many other diseases and conditions listed in the specification. The present sequence represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             includes atherosclerosis, bursitis, cirrhosis, hepatitis, psoriasis, cancers (e.g. lymphoma, melanoma, brain cancer or breast cancer), Cushing's syndrome, Alzheimer's disease, acquired immunodeficiency
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8.3%; Score 164.5; DB 5; Length 328; llarity 21.7%; Pred. No. 1.6e-08; Conservative 41; Mismatches 115; Indels 151; Gaps

15;

----YLLY--CPCMGRFGNQADHFLGSLAFAK 36

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18
                                                            ---ODVPSLEG 210
                                                                                                                                                                                                                                                                       315
                                                                                                                                                                                                                                                                                       152 REQWSQRFSPKEHPVLALPGAPAQFPVLEEHRPLQKYMV----WSDEMVKTGEAQIHAH 206
                                                                                                                                                                                   THWPPEKRVAYCFEVAAQRSPDKKTCPMKEGNPFGPFWDQFHVSFNKSELFTGISFSASY 151
37 LLNRT----LAVPPWIEYQH-HKPPFTNLHVSYQKYFKLEPLQAYHRVISLEDFMEKLAP 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmentel biology and in elucidating cell signalling and cell-cell interactions in higher enkaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIG175, ABLIG175) and the encoded proteins (ABBS7737-ABBS7072). The sequence data for this patent did not form part of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                       267 IQRAVKLWVRSLDAQSVYVATDSESYVPELQQLFKGKVKVVSLKPE------VAQ
                                                                                                                                                                                                                207 LVRPYVGIHLRIGSDWKNACAMLKDGTAGSHFMASPQCVGYSRSTAAPLIMTMCLPDLKE
                                                                                                                          ------GPFIDOVYV-----------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila; developmental biology; cell signalling; insecticide; pharmacentical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 36192; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                         183 LGGPYLGVHLR------RKDFIWGHR--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster polypeptide SEQ ID NO 36192
                                                                                                                                                                                                                                                                                                                                                 316 VDLYILGQADHFIGNCVSSFTAFVKRERDLQG 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                  ABB69800 standard; protein; 490 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Li PWD,
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11-JUL-2000; 2000US-00614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-656860/75
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                                                                                                   92
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                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 14
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3 AGSWDPAG---

Local Similarity les 85; Conserv

Matches

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                                                                                                                                                                                                                                                                                 244
                                                                                                                                                            130
                                                                                                                                                                                                                        190
                                                                                                                                                                                                                                                     107 ---AAQRSPDKKTCPMKEGN-PFGPFWDQFHVSFNKSELFTGISFSAS-----YREQW 155
                                                                                                                                                                                                                                                                                                              211
                                                                                                                                                                                                                                                                                                                                 250 STAAPLIMIMCLPDLKEIQRAVKLWVRSLDAQSVYVATDSESY-VPELQQLFKGKVKVVS 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                    285 MRFARRLEQVAADFRRQALDTTDASAGVORPAMWELERPKRNAKGGDYLCAHLRRGDFVR 344
                                                                                                                                                        71 AVYILYDVNISEGFNLRRDVYIRMAVFVRRLQRRRRFRHVRLVLPPWPRLYHWHSQGLQQ
                                                                                                                                                                                            60 LHVSYQKYFKLEPLQAYHRVISLEDFM--EKLAPTHWPPEKRVAYCFEV-----
                                                                                                                                                                                                               191 FRDKFERVTDK---PCSEGSLSGGPLLQQAELRVGR---FHCVRFQGSAGLLEKLLREAI
                                                                                                                                                                                                                                                                                                              156 SQRFSPKEH----PVLALPGAPAQFPVLEEHRPLQKYMVWSDEMVKTGEAQIHAHLVRPY
                                                                                                                                                                                                                                                                                                                                                                        212 VGIHLR---IGSDWKNACAMLKDGTA-------GSHFMASPQCVGYSR
                                                                                                                                  9 AGYLLYCPCMGR-FGNQADHFLGSLAFAKLLNR-----TLAVPPWIEYQH-HKPPFTN
printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           309 LKPE------VAQVDLYILGQADHFIGNCVSSFTAFVKRERDLQG 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 8.1%; Score 159.5; DB 4; Length 490; Best Local Similarity 22.4%; Pred. No. 1.1e-07; Matches 92; Conservative 55; Mismatches 159; Indels 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster protein, SEQ ID 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 125; 57pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SYGN ) SYNGENTA PARTICIPATIONS AG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADS96504 standard; protein; 490
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2004-376203/35.
N-PSDB; ADS96503.
                                            Sequence 490 AA;
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The present invention relates to a method for identifying a compound that inhibits the activity of a protein essential for Drosophila viability. The method comprises: (a) expressing in a recombinant host a DNA sequence encoding a protein essential for Drosophila viability, (b) testing compounds suspected of having the ability to inhibit the activity of the protein expressed in (a); and identifying a compound tested in identifying a compound that inhibits the activity of the protein. The method is useful in identifying a compound that inhibits the activity of a protein essential for brosophila viability, antihelminthic or acaracidal ectoparasiticidal, antihelminthic or acaracidal agent. The present sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   250 STAAPLIMIMCLPDLKEIQRAVKLWVRSLDAQSVYVATDSESY-VPELQQLFKGKVKVVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 LHVSYOKYFKLEPLQAYHRVISLEDFM--EKLAPTHWPPEKRVAYCFEV-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels 105;
                                                                                                                                                                                                                                                                                                                                                                                    / Match B.1%; Score 159.5; DB 8; Length 490; Local Similarity 22.4%; Pred. No. 1.1e-07; les 92; Conservative 55; Mismatches 159; Indels 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     212 VGIHLR---IGSDWKNACAMLKDGTA-----
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                                                                                                                                                                                                                                                                                                                                                Sequence 490 AA;
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Matches
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Sequence 1, Appli Sequence 478, App Sequence 2, Appli

Sequence 12149, A Sequence 13434, A Sequence 1820, Ap

Sequence 18 Sequence 7,

Sequence 15545, Sequence 12286, Sequence 426, Sequence 2,

7, Appli 33, Appl 12608, A Appli

Sequence

Sequence

Sequence

Sequence 191, App

Sequence

Sequence Sequence Sequence Seguence Sequence

Sequence:

Run on:

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Sequence 13022, A Sequence 12127, A Sequence 16285, A Sequence 15785, A Sequence 15547, A Sequence 573, App Sequence 17508, A
                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 11464, Sequence 12044, Sequence 16387,
                                                                                                                                                                            US-09-291-293A-2

US-09-291-293A-2

US-09-949-016-15286

US-09-949-016-15286

US-09-949-016-12149

US-09-949-016-13143

US-09-540-236-1820

US-09-590-016-1360-1

US-09-949-016-12608

US-09-949-016-15698

US-09-949-016-15698

US-09-949-016-15698

US-09-949-016-16188

US-09-949-016-1617

US-09-949-016-1617

US-09-949-016-1617
   US-09-270-767-13022
US-09-949-016-12127
US-09-949-016-16285
US-09-949-016-13785
US-09-949-016-15547
US-09-902-540-573
US-09-949-016-15547
                                                                                                                             US-09-103-840A-1
US-09-614-221A-478
US-09-103-840A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech) CURRENT APPLICATION DATA: US/08/978,741 FILING DATE: 26-No. 6100076-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Yang Wang, Michael W. Spellman
TITLE OF INVENTION: O-Fucosyltransferase
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 16, Application US/08978741; Patent No. 6100076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/792498
FILING DATE: 31
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REPERENCE/DOCKET NUMBER: P104
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
TELEFAX: 650/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39,044
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                       5591
10357
12665
12665
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2768
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 incl
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US-08-978-741-16
         186
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-MODEL=frame+ pln.model -DEV=xlh
-GeJCgDl2_1/USPTO spool | 1/USPO74954/runat_25102005_105433_6415/app_query.fasta_1.917
-Q=/CgDl2_1/USPTO spool | 1/USPO74954/runat_25102005_105433_6415/app_query.fasta_1.917
-D=16816826 | Patente NA -QPMT=fastap -SUPFIX=rni -MINMATCH=0.1 -LOOPCI=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODB=LOCAL -OUTFMT=pto -NORM=ext -HEAPBIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09774954 @CGN_1 1_116 @runat_25102005_105433_6415 -NOPU=6 -ICPU=3
-NO_MMAD -LARREQUERY -NEG SCORES=0 -WAIT -DSPBILOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THREAPS=1 -XGAPDP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DBLDCR=6 -DBLEXT=7
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Sequence 7, Appli
Sequence 8, Appli
Sequence 1433, A
Sequence 30507, A
Sequence 28905, A
                                                                                                                               October 26, 2005, 08:18:39 ; Search time 320.031 Seconds (without alignments) 1866.199 Million cell updates/sec
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// cgn2 6/ptodate/1/ina/5B_COMB.seq:*
// cgn2 6/ptodate/1/ina/6A_COMB.seq:*
// cgn2 6/ptodate/1/ina/6B_COMB.seq:*
// cgn2 6/ptodate/1/ina/PCTUS COMB.seq:*
// cgn2 6/ptodate/1/ina/PCTUS COMB.seq:*
// cgn2 6/ptodata/1/ina/packflles1.seq:*
                              GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                   - nucleic search, using frame_plus_p2n model
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US-09-333-729A-16
US-08-978-741-4
US-09-333-729A-6
US-09-333-729A-2
US-08-978-741-1
US-08-978-741-7
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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Match Length DB
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Perfect score:
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Jatabase

Result No.

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ProlysGluHisProValleuAlaLeuProGlyAlaProAlaGlnPheProValleuGlu 180
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Matches:
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                                                 2.04e-234
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     ; LENGTH: 1100 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
US-08-978-741-16
                                                       Percent Similarity:
Best Local Similarity: 1
Query Match:
DB:
                                            Alignment Scores:
Pred. No.:
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1 Met Prohladi yserTrpAspProhladi ytyrLeuleuTyrCysProCysMetdiyarg	1 Met Prohladi ysertrphasprohladi ytyrLeuleutyrCysProCysMetdiyarg	1 Met Prohladiy SertrpAspProhladiy Tyrleuleutyr CysProcysMetdly Argin [1] [1] [1] [1] [1] [1] [1] [1] [1] [1]	1 MetProalaGlySerTrpAspProalaGlyTyrLeuLeuTyrCysProcysMetGlyArg 2		2.04e-234 1979.00 100.00% 7: 100.00% 3.3	iation US/0933729A iang an Michael W. an Michael W. an Windber Use 199-06-15 NUMBER: US/09/333,729A NUMBER: US 08/798,741 1997-11-26 OS: 21 2.04e-234 Length: 199.00 Matches: 100.00\$ Mismatches: 100.00\$ Indels: 3.00.00\$ Longervative: 100.00\$ Mismatches: 100.00\$ Mismatches: 100.00\$ Mismatches: 100.00\$ Mismatches: 100.00\$ Mismatches: 100.00\$ Mismatches: 100.00\$ Mismatches:	spGluPhe 365	rgAspLeuGlnGlyArgProSerSerPhePheGlyMetAspArgProProLys 360 [InalaAspHisPheIleGlyAsnCysValSerSerPheThrAlaPheValLys 340
1	MetProAlaGlySerTrpAspProAlaGlyTyrLeuLeuTyrCysProCysMetGlyArg MetProAlaGlySerTrpAspProAlaGlyTyrLeuLeuTyrCysProCysMetGlyArg MetProAlaGlySerTrpAspProAlaGlyTyrLeuLeuTyrCysProCysMetGlyArg ATGCCGGGGGCTCCTGGGACCCGGCGGCGGTTACCTGCTCTACTGCGCTGCTGGGGGGCG ATGCCGGGGGCTCCTGGGCGCGGCGGCGGCGGTTACCTGCTCTACTGCGCCTGCTGGGGGGCGCGTTACTGGGGGGGG	19-774-954-2 (1-365) x US-09-333-729A-16 (1-1100)	09-774-954-2 (1-365) x US-09-333-729A-16 (1-1100) 1 MetProAlaGlySerTrpAspProAlaGlyTyrLeuLeuTyrCysProCysMetGlyArg 2	09-774-954		RESULT 2 10S-09-333-7294-16 1Sequence 16, Application US/09333729A 1Sequence 16, Application US/09333729A 1Sequence 16, Application US/09333729A 1Sequence 16, Application US/09333729A 1SEGNERAL INCRANTION: APPLICANT: Wangy Yang APPLICANT: Spellman, Michael W. TILE REFERENCE: Pl041PlD-Substitute PILE REFERENCE: P1041PlD-Substitute PILE REFERENCE: P1041PlD-Substitute CURRENT PELLON NUMBER: US/09/133,729A 1SELOR PILING DATE: 1999-06-18 1PRIOR PILING DATE: 1999-06-	Oy 361 LeuArgAspGluPhe 365 Db 1081 CTGCGGACGATTC 1095 RESULT 2 US-09-333-729A-16 Sequence 16, Application US/0933729A Sequence 16, Application US/0933729A PAPLICANT: Wangy ang APPLICANT: Wangy ang APPLICANT: Spellman, Michael W. TILE REFERENCE: PLO4FELD-Subscituce TILE REFERENCE: PLO4FELD-Subscituce CURRENT APLICATION NUMBER: US/09/33, 729A CURRENT APLICATION NUMBER: US 08/798, 741 PRIOR PLICATION NUMBER: US 08/798, 741 PRIOR FILING DATE: 1999-06-15 NUMBER OF SEQ ID NOS: 21 LENGTH: 1100 LENGTH: 1100 LENGTH: 1100 CORGANISM: Homo Sapien US-09-333-729A-16	rphephedlymetaspargproprolys 360	94alserserPherhrAlaphevallys 340 1GH(
	yevallysvalvalstandinglinglinglinglinglinglinglinglinglingl	yevaluysvalvalserLeuLysroGuvalaadinguyaniyille 320	yevaluysvalvalserLeuLyeroGluvalAnlaGluvalAnlaGluvalitie	yevaluysvalvalserLeuLysvalvalserScaluvalAtlaGinvalAfaptera	301 Lysdilysvallysserleutystrollystalitystics	301 1ysGllypsVallysPsTellUpsProGluydaAdaGluydAsBprogluydAsBprogluydAsBprogluydAsBprogluydAsBprogluydAsBprogluydAsBprogluydAsBprogluydAsBprogluydAsBprogluydAsBprogluydAsBprogluydAsBprogluydAsBprogluydasBprogluy	301 LysGlyLysYalLysYalYalScrLeubyBroGlyDahadsInValAbburdhyBris 320 1/10	301 LysGlyLysValLysValValSerLeuLysProGluValAlacInValAspleuLyrile 32	2. STITINITE TO THE PROPERTY OF THE PROPERTY O

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26-No. 610076-1997
                 PILING DATE: 26-No. 61000/0-12.CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/792498
FILING DATE: 31
ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REGISTRATION NUMBER: 91,044
REBERENCE/DOCKET NUMBER: 91,044
RELEPRANCE 560/225-1489
TELEPRANCE 650/225-1489
INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
LENGTH: 1300 base pairs
LENGTH: 1300 base pairs
STRANDEDNESS: Single
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            APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/08978741
| Patent No. 610076
| GENERAL INFORMATION: GENERAL INFORMATION: TITLE OF INVENTION: O-FUCOSyltransferase NUMBER OF SEQUENCES: 17
| CORRESPONDENCE ADDRESS: ADDRESSEE: Genentech, Inc. STREET: 1 DNA Way
| CITY: South & Prancisco | STATE: California | COUNTRY: USA | CONTRY: USA | CONTRY: USA | COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: 1BM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS COFTWARE: WinPatin (Genetech) CURRENT APPLICATION DATA:
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GCCCAGATTCATGCCCACCTTGTCCGGCCCTATGTGGGCATTCATCTGCGCATTGGCTCT 795
                                               AspTrpLysAsnAlaCysAlaMetLeuLysAspGlyThrAlaGlySerHisPheMetAla
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                        GACTGGAAGAAGGCCTGTGCCATGCTGAAGGACGGGACTGCAGGCTCGCACTTCATGGCC
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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APPLICANT: Wang, Yang
APPLICANT: Spellman, Michael W.
TITLE OF INVENTION: O'bucosyltransferase
FILE REFERENCE: P1041P1D1-Substitute
CURRENT APPLICATION NUMBER: US/09/333,729A
CURRENT PILING DATE: 1999-06-15
PRIOR FILING DATE: 1997-11-26
NUMBER OF SEQ ID NOS: 21
LENGTH: 1300
                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/09333729A Patent No. 6270987 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                            ) OTHER INFORMATION: Plasmid insert. US-09-333-729A-6
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ORGANISM: Artificial Sequence
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Best Local Similarity: 1
Query Match:
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US-09-333-729A-6
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ProLysGluHisProValLeuAlaLeuProGlyAlaProAlaGlnPheProValLeuGlu
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                                                                         LeuPheThrGly11eSerPheSerAlaSerTyrArgGluGlnTrpSerGlnArgPheSer
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APPLICANT: Wang, Yang
APPLICANT: Spellman, Michael W.
TITLE OF INVENTION: O-Fucosyltransferase
FILE REFERENCE: Pl041P1D1-Substitute
CURRENT APPLICATION NUMBER: US/09/333,729A
CURRENT FILING DATE: 1999-06-15
PRIOR FILING DATE: 1997-11-26
NUMBER OF SEQ ID NOS: 21
LENGTH: 1514
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CORGANISM: Homo Sapien
US-09-333-729A-2
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Matches:
Conservative:
Mismatches:
Indels:
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Winheatin (Genentech) CURENT APPLICATION DATA: APPLICATION NUMBER: US/08/978,741
FILING DATE: 26-No. 610076-1997
CLASSIFTATION: 435
PRIOR APPLICATION NUMBER: 08/792498
FILING APPLICATION NUMBER: 08/792498
FILING APPLICATION NUMBER: 33
ATTORNEY/AGENT INFORMATION:
NAME: SVODGA, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: 91041P1
TELECOMMUNICATION INFORMATION:
TELENSWER STORMEN NUMBER: PLANTER STORMEN 
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          GENERAL INFORMATION:
APPLICANT: Yang Wang, Michael W. Spellman
TITLE OF INVENTION: O-Fucosyltransferase
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1514 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
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1979.00
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CITY: South San Francisco
STATE: California
COUNTRY: USA
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	RESULT 7 US-08-978-741-5 Sequence 5, Application US/08978741 ; Sequence 5, Application US/08978741 ; Patent No. 6100076 ; GENERAL INFORMATION: ; APPLICART: Yang Wang, Michael W. Spellman ; TITLE OF INVENTION: O-Fucosyltransferase	NUMBER OF SEQUENCES: 17 ; CORRESPONDENCE ADDRESS: ; ADDRESSEE: Genentech, Inc. ; STREET: 1 DNA Way ; CITY: South San Francisco ; STATE: California ; COUNTRY: USA ; COMPUTER PRADABLE FORM:	MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible COMPUTER: STATEM: PC-DOS/MSD-DOS COFTWARE: Winderin (Geneticch) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/978,741 CLASSIPTCATION: 435.No. 6100076-1997		FELEMENTS 650/225-1889 TELEMENTS 650/952-9881 INPORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS: TYPE: Nucleic Acid STRANDEDNES: Single TOPOLOGY: Linear	Alignment Scores: Alignment Scores: Pred. No.: Score: 1979.00 Matches: 365 Score: 1979.00 Matches: 365 Serent Similarity: 100.00\$ Conservative: 0 Best Local Similarity: 100.00\$ Mismatches: 0 Ouery Match: 100.00\$ Mismatches: 0	-09-774-954-2 (1-365) x US-08-978-741-5 (1-11284) 1 MetProAlaGlySerTrpAspProAlaGlyTytLeuLeuT 4236 ATGCCGCGGGGCTCCTCGGACCCGGCGGTTACCTGCTCT 21 PheGlyAsnGlnAlaAspHisPheLeuGlySerLeuAlaP 4296 TTCGGSAACCAGGCCGATCACTTCTTGGGCTCTCTGGACTCTTGGGCTTTTTTTT
Score: 365 1979.00 Matches: 365 Secore: 365 Percent Similarity: 100.00\$ Conservative: 0 Best Local Similarity: 100.00\$ Mismatches: 0 Ouery Match: 3 100.00\$ Indels: 0 Ouery Match: 3 Ouery Match: 0 Ouery Match: 3 Ouery Match: 0 Ouery Matchine Ouery Match: 0 Ouery Matchine Oue	21 PheclyAsnGlnAlaAspHisPheLeuGlySerLeuAlaPheAlaLysLeuLeuAsnArg	Db 121 ACCTTGGCTGTCCTTGGATTGAGTACCAGCATCACAGCCTCTTTCACCAACCTC 180	101 AlaTyrCysPheGluValAlaAlaGlnArgSerProAspLysLysThrCysProMetLys	141 LeupherhrGly11eSerPheSerAlaSerTyrArgGluGlnTrpSerGlnArgPheSer 421 CTTTTTACAGGCATTCCTTCTTTTTTTTTTTTTTTTTTT	Oy 181 GlubisArgProLeuGlnLysTyrMetValTrpSerAspGluMetValLysThrGlyGlu 200	Qy 221 AspTrDLysAshAlaCysAlaMetLeuLysAspGlyThrAlaGlySerHisPhemetAla 240 Db	Oy 261 LeuproAspLeulysGluileGlnArgAlaValLysLeuTrpValArgSerLeuAspAla 280

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GENERAL INFORMATION:
APPLICANT: Yang Wang, Michael W. Spellman
TITLE OF INVENTION: O-Fucosyltransferase

Sequence 7, Application US/08978741 Patent No. 6100076

US-08-978-741-7

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83 GluhsppheMetGluLysLeuAlaProThrHisTrpProProGluLysArgValAlaTyr 102
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Matches:
Conservative:
Mismatches:
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
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                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTHARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,741
FILING DATE: 26-No. 6100076-1997
CLASSIFFCATION NUMBER: 08/792498
FILING DATE: 31
ATTORNEY/AGENT INFORMATION:
NAME: SYCHOGA, CTAIG G.
REGISTRATION NUMBER: 39,044
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P1041P1
TELECHONE: 650/255-1489
TELEFAX: 650/952-9881
TELEFAX: 650/952-9881
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TELEFAX: 650/952-9881
                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
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NUMBER OF SEQUENCES:
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Best Local Similarity:
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GlnAlaAspHisPhelleGlyAsnCysValSerSerPheThrAlaPheValLysArgGlu 342
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                                    ArgAspLeuGlnGlyArgProSerSerPhePheGlyMetAspArgProProLysLeuArg
     GAGGATTTCATGGAGAAGCTGGCACCCACCCACCCACGCCCCTGAGAAGCGGGTGGCATAC
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GlnAlaAspHisPheIleGlyAsnCysValSerSerPheThrAlaPheValLysArgGlu
                                       482 AGGCCACTACAGAAGTACATGGTATGGTCAGACGAAATGGTGAAGACGGGAGAGGCCCCAG
                                                                                         LysAsnAlaCysAlaMetLeuLysAspGlyThrAlaGlySerHisPheMetAlaSerPro
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Conservative:
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                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Wang Yang
APPLICANT: Spellman, Michael W.
APPLICANT: Spellman, Michael W.
ITLE OF INVENTION: O-Fucosyltransferase;
FILE REFERENCE: P1041P1D1-Substitute
CURRENT APPLICATION WUMBER: US/09/333,729A;
CURRENT FILING DATE: 1999-06-15
PRIOR APPLICATION WUMBER: US 08/798,741
PRIOR PILING DATE: 1997-11-26
; NUMBER OF SEQ ID NOS: 21
                                                                                                                                                                                                                                                                                                                                   RESULT 9
US-09-333-729A-8
US-09-333-729A-8
; Patent No. 6270987
; GENERAL INFORMATION:
; APPLICANT: Wang, Yang
; APPLICANT: Spellman, Michael W.
; TITLE OF INVENTION:
; TITLE OF INVENTION:
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1844.00
100.00%
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CRGANISM: Homo Sapien
US-09-333-729A-8
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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                                     APPLICANT: Homburger et al.
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Serence: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 14353
LENGTH: 1320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                179 LeuGluGluHisArgProLeuGlnLysTyrMetValTrpSerAspGluMetValLysThr
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Matches:
Conservative:
Mismatches:
Indels:
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US-09-270-767-14353
; Sequence 14353, Application US/09270767
; Patent No. 6703491
                                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-14353
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Batent No. 6703491

GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT FILING NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 30507
LENGTH: 722
                                                                                                                                                                                                                                                                                       215 HisleuArgIleGlySerAspTrpLysAsnAlaCysAlaMetLeuLysAspGlyThrAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 CATCTGCGCAACGGTATCGATTGGGTGAGGCCTGTGAGCACGTCAAGGAT-----
                                                                                                                                                                    ThrMetCysLeuProAspLeuLysGluIleGlnArgAlaValLysLeuTrpValArgSer
                                                                                                                                                                                                                                                              Leu-------AspAlaGlnSerValTyrValAlaThrAspSerGlu
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837 GAGCTCTGCATGCCTCCAAGGAGGCGATCATCCGCCAGCTAAAGAGAAACATTAAGAAC
                                                                                                                                                                                                                                                                                                                                                             291 SerTyrValProGluLeuGln---GlnLeuPheLysGlyLysValLysValValSerLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        330 AsnCysValSerSerPheThrAlaPheValLysArgGluArgAspLeuGlnGlyArgPro
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                                                                                                   CTGTTTGCCTCGCCGCAGTGCTTGGGCTATAAAAATGAACGTGGTGCA---CTCTACCCG
                        --- AGCCAGCAT
                                                                     PheMetAlaSerProGlnCysValGlyTyrSerArgSerThrAlaAlaProLeuThrMet
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Conservative:
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318 LeuTyrIleLeuGlyGlnAlaAspHisPheIleGlyAsnCysValSerSerPheThrAla 337
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                     US-09-270-767-13022/c
US-09-270-767-13022/c
US-09-270-767-13022/c
Sequence 13022, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
GENERAL INFORMATION:
FILE REFERENCE:
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION UNMER: 1999-03-17
CURRENT APPLICATION UNMER: 1999-03-17
SOFTWARE: Patentin Ver. 2.0
SSEQ ID NOS: 62517
SSEQ ID NO 13022
SEQ ID NO 13022
                                                                                                                                                                                                                                                                                                                                                                                                                 279 AspAlaGlnSerValTyrValAlaThrAspSerGluSerTyrValProGluLeuGln---
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Matches:
Conservative:
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; ORGANISM: Drosophila melanogaster
US-09-270-767-13022
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1777 ---CCCAAGGAAAAGGAT 1763
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186.00
67.44%
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Best Local Similarity:
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; ORGANISM: Human
US-09-949-016-12127
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Pred. No.:
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                                                       289
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                                                                                                                                                                                                  307 ValSerLeuLysProGluValAlaGlnValAspLeuTyrIleLeuGlyGlnAlaAspHis 326
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173 AGCCAGCATCTGTTTGCCTCGCCGCAGTGCTTGGGCTATAAAAATGAACGTGGTGCA--- 229
                                                                                                                                            288 AspSerGluSerTyrValProGluLeuGln---GlnLeuPheLysGlyLysValLysVal 306
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US-09-270-767-28905/c
Sequence 28905, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
PAPLICANT: Homburger et al.
TITLE OF INVENTION:
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
TITLE OF INVENTION: NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 28905
LENGTH: 998
                                            255 LeuThrMetThrMetCysLeuProAspLeuLysGluIleGlnArgAlaValLysLeuTrp
                                                                                    347 GlyArgProSerSerPhePheGlyMetAspArgProProLysLeuArgAsp 363
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Matches:
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US-09-270-767-28905
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RESULT 15
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| Sequence 16285, Application US/09949016
| Patent No. 6812339
| GENERAL INFORMATION:
| APPLICANT: VEWTER, U Craig et al. APPLICANT: VEWTER, U CLAIG et al. APPLICANT: VEWTER, U CLOU3.07
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
| FILE REPRENCE: CLOU3.07
| CURRENT APPLICATION NUMBER: US/09/949,016
| CURRENT FILING DATE: 2000-04-14
| PRIOR APPLICATION NUMBER: 60/231,768
| PRIOR FILING DATE: 2000-10-03
| PRIOR FILING DATE: 2000-09-08
| NUMBER OF SEQ ID NOS: 207012
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO 16285
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; ORGANISM: Human
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Q920W5 Q9JL28 FTSK_STRPN FTSK_STRR6 Q7YTAS	ALIGNMENTS	PRT; 61 AA.	45, Created) 45, Last sequence update) 45, Last annotation update) n O-fucosyltransferase 1 (EC e) (O-Fucr-1) (Fragment).	(Chinese hamster). Chordata; Craniata; Vert. Rodentia; Sciurognathi;	PubMed=11524432; DOI=10.107, Shi S., Harris R.J., Spellm pidermal growth factor-like and expression of a novel Gi	0348/2001). 358148; ; post-translationa 3).	023546; R.F., Spellman M.W -fucose:polypoptid nked fucose to EGF 6).	ization of a nese hameter nese hameter 8(1998). reaction tha a conserved nsfers an alp rine hydroxy rine hydroxy her divalent m, magnesium
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN-FYB/N-3: TISSUE-Mammary gland;

MEDLINE=22188257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Rusner R.D., Collins F.S., Wagner L., Shemem C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max. S.I., Wang J., Hsieh F.,

A blatchen's C., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A blatchen's C., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J. Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,

A stapleton M., Soares M.B., Bonnaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J. Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,

A stapleton M.S., McGranan K.J., Malek J.A., Gunaratne P.H.,

Brownstein M.J., McGranan K.J., Malek J.A., Garia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

B hakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

R Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

R Schnerch A., Schein J.E., Jonna M., Marra M.A.;

Schnerch A., Schein J.E., Jonna M., Marra M.A.;

R Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                1 RLAGSWDLAGYLLYXPXMGRFGNQADHFLGSLAFAKLXVRTLAVPPWIEYQHHKPPFTNL 60
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- FUNCTION: Catalyzes the reaction that attaches fucose through an O-glycosidic linkage to a conserved serine or threonine residue in EGF domains (BP similarity).
-!- CATALYTIC ACTIVITY: Transfers an alpha-L-fucosyl residue from GDP-beta-L-fucose to the serine hydroxy group of a protein acceptor.
                                                                                                                                                                                                                                                                                                                   1 RLAGSWDLAGYLLYXPXMGRFGNQADHFLGSLAFAKLXVRTLAVPPWIEYQHHKPPFTNL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
25-OCT-2004 (Rel. 45, Last sequence update)
GDP-fucose protein O-fucosyltransferase 1 precursor (EC 2.4.1.221)
(Peptide O-fucosyltransferase) (O-FucT-1).
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TaxID=10090;
-i- PTM: N-glycosylated.
-i- SIMILARITY: Belongs to the glycosyltransferase 68 family.
Direct protein sequencing; Pucose metabolism; Glycoprotein;
Glycosyltransferase; Manganese; Transferase.
NON TER
                                                                                                                                                                                                       ch 98.2%; Score 320; DB 1; Length 61; 
1 Similarity 100.0%; Pred. No. 3.2e-35; 
61; Conservative 0; Mismatches 0; Indels
                                                                                                                                     61 61
61 AA; 6951 MW; E9507AE60018F23A CRC64;
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J. Biol. Chem. 276:40338-40345(2001).
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STAIN-(SCIPL)64; TISSUE-Retina;
STAIN-(SCIPL)65; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninoi P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Potential.
GDP-fucose protein O-fucosyltransferase
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01-ORT-2003 (TrEMBLrel. 25, Last annotation update)
Mus musculus adult retina cDNA, RIKEN full-length enriched library,
clone:A930028F21 product:protein O-fucosyltransferase 1, full insert
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                     67 N-linked (GlcNAc. .) (Potential).
165 N-linked (GlcNAc. .) (Potential).
44688 MW, D982104E95E5CF3B CRC64;
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-!- COFACTOR: Manganese (By similarity).
-!- PATHWAY: Glycosylation.
-!- SIMILARITY: Belongs to the glycosyltransferase 68 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 393;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 305; DB 1; Length 39:
Pred. No. 2.3e-32;
0; Mismatches 5; Indels
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STRAIN-GS7BL/61, TISSUB-Retina;
MEDLINE-21085660; PubMed=11217851; DOI=10.1038/35055500;
RIKEN FARYOM CONSORTIUM;
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91.8%;
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Best Local Similarity 91.8
Matches 56; Conservative
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J. Biol. Chem. 276:40338-40345(2001).
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SEQUENCE 395 AA; 44983 MW; 2
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                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat).
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Adachi J., Aizawa T., Arakawa T., Bono H., Carninci P., Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Adachi J., Aizawa K., Akimura T., Hara A., Hashizume W., Hukuda S., Furuno M., Hiramoto K., Hiraoka T., Hirozane T., Hayashida K., Ishii Y., Itoh M., Kagawa I., Kasukawa T., Karoh F., Komdo S., Konno H., Kowia T., Konjima Y., Kondo S., Konno H., Kowia M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Oksato N., Oksato N., Oksato H., Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M., Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T., Towaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.; Tamaka T., Tamaka T., Tamaka M., Muramatsu M., Hayashizaki Y.; Embl. AKO44629; BAC32009.1; --
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STRAIN=C57BL/6J; TISSUE=Retina;
STRAIN=C57BL/6J; TISSUE=Retina;
STRAIN=C57BL/6J; TISSUE=Retina;
Shibata K., Itch M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., A. Shibata K., Itch M., Aizawa K., Kitsunai T., Tashiro H., Itch M., Akiyama J., Nishih K., Kitsunai T., Tashiro H., Itch M., A. Yamamoto R., Matsuncoto H., Sakaquchi S., Ikegami T., Harada A., A. Yamamoto R., Matsuncoto H., Sakaquchi S., Ikegami T., Kashiwagi K., A. Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Matshiki M., A. Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y., A. Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; RIKEN integrated sequence analysis (RISA) system 384-format genome Res. 10:1757-1771(2000).
                                                                      SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-Retina;
The FANTOM Consortium.
The RIKEN Genome Exploration Research Group Phase I & II Team;
The Manalysis of the mouse transcriptome based on functional annotation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; Muramatsu M., Hayashizaki Y.; Muramatsu M., Hayashizaki Y.; Muramatsu of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29 RSAGSWDLAGYLLYCPCMGRFGNQADHFLGSLAFAKLLNRTLAVPPWIEYQHHKPPFTNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 RLAGSWDLAGYLLYXPXMGRFGNQADHFLGSLAFAKLXVRTLAVPPWIEYQHHKPPFTNL
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                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=C57BL/6J; TISSUB=Retina;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Indels
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91.8%; Pred. No. 2.3e-32;
ive 0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO; GO:0005615; C:extracellular space; TAS. GO; GO:0001525; P:angiogenesis; IMP. GO; GO:0006004; P:fucose metabolism; TAS. GO; GO:0007507; P:heart development; IMP. GO; GO:0007399; P:neurogenesis; IMP. GO; GO:0007219; P:Notch signaling pathway; IMP. GO; GO:0001756; P:somitogenesis; IMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glycosyltransferase; Transferase
                                                                                                                                                                                                                                                               60,770 full-length cDNAs.";
Nature 420:563-573(2002).
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Best Local Similarity 91.87
Matches 56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MGI:2153207; Pofut1
Nature 409:685-690(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           393 AA;
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Martinez-Duncker I., Oriol R., Mollicone R.;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ781499; CAH03711.1; -.
GO; GO:0016757; F:transferase activity, transferring glycosyl. . .; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 RIAGSWDIAGYLLYXPXMCRFGNQADHFLGSLAFAKLXVRTLAVPPWIEYQHHKPPFTNL
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                                                                                                                                                                                    Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Modification of epidermal growth factor-like repeats with O-fucose: molecular cloning and expression of a novel GDP-fucose protein O-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9H488; Q14685; Q9BW76;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
25-OCT-2004 (Rel. 45, Last amnotation update)
GDP-fucose protein O-fucosyltransferase 1 precursor (EC 2.4.1.221)
(Peptide O-fucosyltransferase)
                                                                                                                                                                                                                                                                                                                                                                                                                         fucosyltransferases and alpha6-fucosyltransferases: phylogeny and identification of conserved peptide motifs."; Glycobiology 13:1C-5C(2003).
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Wang Y., Shao L., Shi S., Harris R.J., Spellman M.W., Stanley P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                STRAIN=Wistar;
PubMed=12966037; DOI=10.1093/glycob/cwg113;
Martinez-Duncker I., Mollicone R., Candelier J.J., Breton C.,
                                                                                                                                                                                                                                                                                                                                                                                                              "A new superfamily of protein-O-fucosyltransferases, alpha2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92.6%; Score 302; DB 2; Length 395; 90.2%; Pred. No. 5.9e-32; tive 0; Mismatches 6; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44983 MW; 2A85521E22F38920 CRC64;
                                           $5-OcT-2004 (TrEMBLrel. 28, Created)
$5-OcT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Protein-O-fucosyltransferase 1.
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395 AA
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CARBOHYD
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Matches
   SEQUENCE FROM N.A. (ISOFORM 2).

REDINELEZ1388257; Pubbed=12477932; DOI=10.1073/pnas.242603899;

RISURE-Brain;

BEDINELEZ2388257; Pubbed=12477932; DOI=10.1073/pnas.242603899;

RIAUBERT R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

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Buchtins R.P., Jordan H., Moore T., Max. S.I., Wang J., Hsieh F.,

RA Altschul S.F., Jordan H., Moore T., Max. S.I., Wang J., Hsieh F.,

RA Stapleton M.J. Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

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Brownstein M.J., Woffernan K.J., Malek J.A., Gunaratne P.H.,

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Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

R Hahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

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R Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

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                                                                                                                                                                                                                                                                                                                                                                                                              Luna Kes. 3:17-2411996).

Luna Kes. 3:17-2411996).

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A Jones M., Starvides G., Almeida J.P., Babbage A.K., Bagguley C.L.,

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Phillimore B.J.C.T., Prathalingam S.R., Plunb R.W., Ramsay H.,

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DNA Res. 9:99-106(2002).
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MEDLINE=97175972; PubMed=9023546;
Wang Y., Lee G.F., Kelley R.F., Spellman M.W.;
"Identification of a GDP-L-fucose:polypeptide fucosyltransferase and enzymatic addition of O-linked fucose to EGF domains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nogers J.; "The DNA sequence and comparative analysis of human chromosome 20."; Nature 414:865-871(2001).
                                                                                                                                                                                               TISSUE-Bone marrow;

MEDILNE-96281124; PubMed-8724849;

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Nagase T., Schi N., Ishikawa K.-I., Tanaka A., Nomura N.;

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"Prediction of the coding sequences of unidentified human genes. V. The coding sequences of 40 new genes (KIAA0161-KIAA0200) deduced by analysis of CDNA clones from human cell line KG-1.";

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                                                                                                                                                             SEQUENCE OF 46-388 FROM N.A. (ISOFORM 1).
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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FSPKEHPVLALPGARACPOULEHRPLQKYWWSDEMVKTG
EAQIHAHLWYBYVGTHIKISSDWKNAGAMKLOGTAGSHPWA
SPQCVGYSRSTAAPITWTMCLPDLKSIORAVKLWYSLLDAQ
SVYVATDSESYVPELQQLFKGKVKVVSLKPEVAQVDLYILG
QAHFIGNGVSSTAAFVRREDLQGRESSFFGMNRPFKLRD
EF -> RENHSCYTLLFPR (in isoform 2).
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Glycobiology 6:837-842(1996).
-!- FUNCTION: Catalyzes the reaction that attaches fucose through an
O-glycosidic linkage to a conserved serine or threonine residue in
EGF domains.
                                                                                                                 -!- CATALYTIC ACTIVITY: Transfers an alpha-L-fucosyl residue from GDP-beta-L-fucose to the serine hydroxy group of a protein acceptor.
-!- COFACTOR: Manganese.
-!- PATHWAY: GJYCOSYJation.
-!- ALTERNATIVE PRODUCTS:
EVENTE-Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Potential.
GDP-fucose protein O-fucosyltransferase
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                                                                                                                                                                                                                                                                                                                                                                       Isold-09H488-2; Sequence=VSP 001809;
Note=No experimental confirmation available;
Note=No experimental confirmation available;
1-TISSUE SPECIFICITY: Highly expressed in heart, brain, placenta, lung, liver, skeletal muscle, kidney and pancreas.
-:- SIMILARITY: Belongs to the glycosyltransferase 68 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-linked (GlcNAc. . .) (Potential).
N-linked (GlcNAc. . .) (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 90.5%; Score 295; DB 1; Length 388; Local Similarity 91.5%; Pred. No. 5.1e-31; les 54; Conservative 0; Mismatches 5; Indels
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(Rel. 45, Last sequence update)
                                                                                                                                                                                                                                                                                                 Name=1;
IsoId=Q9H488-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, AF375884; AAL09576.1; --
EMBL, BOR002; BAA1497.2; --
EMBL, AL121897; CAC16424.1; --
EMBL, BC000582; AAH0582.1; --
Genew; HOKC:14988; POFUT1.
H-INVDB; HIXO015724; --
MIM; 607491; --
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ID OFUL PANTR
AC QEEVE9;
DT 25-OCT-2004 (1)
DT 25-OCT-2004 (1)
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Glycosyltransferase, Transferase.
SEQUENCE 351 AA, 39576 MW; BF830F61A7296F42 CRC64;
                                                                   52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          378 378 378 AA;
                                                                                                                                                                                                                                                                        Name=pofut1;
Bos taurus (Bovine)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                        391 AA;
                                          Query Match
Best Local Similarity
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9913;
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                                                                                                                                                                                                                                                                                                                Mammalia, Eut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=POFUT1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q7YRZ3;
                                                                                                                                                                                                          Q7YRE7;
                                                                                                                                                                                          Q7YRE7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q7YRZ3
                                                          Best Loca
Matches
                                                                                                                                                                  RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27YRZ3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
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                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                  modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Loriol C., Germot A., Dupuy F., Maftah A.;
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AX344581; AAQ02333.1;
GO; GO:0016757; F:transferase activity, transferring glycosyl. . .; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 AGSWDLAGYLLYXPXMGRFGNQADHFLGSLAFAKLXVRTLAVPPWIEYQHHKPPFTNLH 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glycobiology 13:1C-5C(2003).

-!- FUNCTION: Catalyzes the reaction that attaches fucose through an O-glycosidic linkage to a conserved serine or threonine residue in BGF domains (By similarity).

-!- CATALYTIC ACTIVITY: Transfers an alpha-L-fucosyl residue from GDP-beta-L-fucose to the serine hydroxy group of a protein acceptor.

-!- COFACTOR: Manganese (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Potential.
GDP-fucose protein O-fucosyltransferase
     25-OCT-2004 (Rel. 45, Last annotation update)
GDP-fucose protein O-fucosyltransferase 1 precursor (EC 2.4.1.221)
(Peptide O-fucosyltransferase) (O-FucT-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
Bovinae, Bos.
                                                                                                                                                                                 "A new superfamily of protein-O-fucosyltransferases, alpha2-fucosyltransferases: phylogeny and identification of conserved peptide motifs.";
                                                            Pan troglodytes (Chimpanzee).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AJ701500; CAH03712.1; -.
Fucose metabolism; Glycoprotein; Glycosyltransferase; Manganese;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-linked (GlcNAc. . .) (Potential)
N-linked (GlcNAc. . .) (Potential)
                                                                                                                            SEQUENCE FROM N.A.
PubMed=12966037; DOI=10.1093/glycob/cwg113;
Martinez-Duncker I., Mollicone R., Candelier J.J., Breton C.,
                                                                                                                                                                                                                                                                                                                       -i- PATHWAY: Glycosylation.
-i- SIMILARITY: Belongs to the glycosyltransferase 68 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 388;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90.5%; Score 295; DB 1; Length 38
91.5%; Pred. No. 5.1e-31;
tive 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3FACCCA434D02415 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 351 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last seq
01-WAR-2004 (TrEMBLrel. 26, Last ann
Protein O-fucosyltransferase lb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   388 AA; 43955 MW;
                                                Name=POFUT1; Synonyms=FUT12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26
388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Signal, Transferase.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62
                                                                                                   NCBI_TaxID=9598;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=pofut1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
SEQUENCE
                                                                                                                                                                       Oriol R.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 O7YRE6;
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Matches
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EMBL, A3567917, CAD99201.1, -.
GO; GO:0016757, F:transferase activity, transferring glycosyl. . .; IEA.
Glycosyltransferase; Transferase.
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                                                                                                              4 GSWDLAGYLLYXPXMGRFGNQADHFLGSLAFAKLXVRTLAVPPWIEYQHHKPPFTNLH 61
                                                                                                                                              30 GSWDPAGYLLYCPCMGRFGNQADHFLGSLAFAKLLNRTLAVPPWIEYQHHKPPFTNVH 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 GSWDLAGYILYXPXMGRFGNQADHFLGSLAFAKLXVRTLAVPPWIEYQHHKPPFTNLH 61
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                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Martinez-Dunker I., Mollicone R., Candelier J.J., Breton C., Oriol "A new superfamily of protein-O-fucosyltransferases, alpha2-fucosyltransferases: phylogeny and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sus scrofa (Pig).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Loriol C., Germot A., Dupuy F., Maftah A.;
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY344580; AAQ02332.1; -
GO; GO:0016757; F:transferase activity, transferring glycosyl.
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Pred. No. 4.5e-30;
1; Mismatches 5; Indels
88.3%; Score 288; DB 2; Length 351; 89.7%; Pred. No. 4e-30; ive 1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42842 MW; 1870DEB0C50713F1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glycosyltransferase; Transferase.
SEOHENCE 391 AA: 44307 MW; 96762AB81A2027AD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                  01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 286; DB 2;
Pred. No. 8e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Identification of conserved peptide motifs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            378 AA
                                                                                                                                                                                                                                                                                                                    391 AA
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01-OCT-2003 (TrEMBLrel. 25, Last seq
01-MAR-2004 (TrEMBLrel. 26, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein O-fucosyltransferase la.
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89.8%;
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Best Local Similarity 89.7%;
Matches 52; Conservative
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PRELIMINARY;
                                                                                            PRELIMINARY;
                                                                                                                                                                                                      Xenopodinae, Xenopus.
NCBL_TaxID=8364;
                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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25-OCT-2004 (
25-OCT-2004 (
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                                                                                                       064080;
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Matches
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QGEV71
                                                                     RESULT 12
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Submitted (UDL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ781503; CAH03714.1; -.
GO; GO:0016757; F:transferase activity, transferring glycosyl. . .; IEA.
Glycosyltransferase; Transferase
SEQUENCE 391 AA; 44277 MW; 4E047D6BB5CDF7FA CRC64;
                                    22 AVSWDPAGYLLYCPCMGRFGNQADHFLGSLAFAKLLNRTLAVPPWIEYQHHKPPFTNLH 80
                       3 AGSWDLAGYLLYXPXMGRFGNQADHFLGSLAFAKLXVRTLAVPPWIEYQHHKPPFTNLH 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 GSWDLAGYLLYXPXMGRFGNQADHFLGSLAFAKLXVRTLAVPPWIEYQHHKPPFTNLH 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30 GSWNPAGYLLFCPCMGRFGNQADHFLGSLAFAPLMNRTLAVPPWIEYQHKPPFTNVH 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gallus gallus (Chicken).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                          SECUENCE FROM N.A.

PubMed=12966037; DOI=10.1093/glycob/cwg113;

Martinez-Duncker I., Mollicone R., Candelier J.J., Breton C.,
Oriol R.;

"A new superfamily of protein-O-fucosyltransferases, alpha2-
fucosyltransferases and alpha6-fucosyltransferases; alpha9-
identification of conserved peptide motifs.";
                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
83.7%; Score 273; DB 2; Length 39:
Best Local Similarity 84.5%; Pred. No. 4.6e-28;
Matches 49; Conservative 3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 83.4%; Score 272; DB 2; Length 38 Best Local Similarity 79.7%; Pred. No. 6.1e-28, Matches 47; Conservative 6; Mamatches 6; Indels
6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oriol R.; Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases. EMBL; 43355754; CAD59738.1; -. Hypothetical protein. SEQUENCE 380 AA; 43316 MW; 83B53B342511811B CRC64;
                                                                                                                                            28, Last sequence update)
28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                        391 AA
0; Mismatches
                                                                                                        PRT;
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01-WAR-2003 (TrEWBLrel. 23, Last seq
01-WAR-2003 (TrEWBLrel. 23, Last ann
Hypotherical protein POFUTI.
Name=POFUTI;
                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                      25-OCT-2004 (TrEMBLrel, 28, Last
Protein-O-fucosyltransferase 1.
                                                                                                                              (TrEMBLrel. 28, (TrEMBLrel. 28,
53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                        PRELIMINARY;
                                                                                                                                                                                           Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                        NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gallus.
NCBI_TaxID=9031;
                                                                                                                                                                                                                               Bovinae; Bos
                                                                                                                                          25-OCT-2004
25-OCT-2004
                                                                                                                                 25-OCT-2004
                                                                                                                                                                                Name=fut12;
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                                                                                                        Q6EV66
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Q8AWB4
 Matches
                                                                                  RESULT 10
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3 AGSWDLAGYLLYXPXMGRFGNQADHFLGSLAFAKLXVRTLAVPPWIEYQHHKPPFTNLH 61
                        18 AGSWDTAGYLLYCPCMGRFGNQAEHFLGALAFARALNRTLAVPPWIEYRHHRPFYTNLH 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 WDSSGYILYCPCMGRFGNQADHFLGSLAFAXMVNRTLVVPPWIVYNHHRPPPYTNVH 76
                                                                                                                                                                                                          25-0CT-2004 (TrEMBLrel. 28, Created)
25-0CT-2004 (TrEMBLrel. 28, Last sequence update)
25-0CT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein.
Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 WDLAGYLLYXPXMGRFGNQADHFLGSLAFAKLXVRTLAVPPWIEYQHHKPPFTNLH
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Name=fut12;

Kenopus tropicalis (Western clawed frog) (Silurana tropicalis).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 380;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 76.7%; Score 250; DB 2; Length 38. Local Similarity 75.0%; Pred. No. 5.6e-25; les 42; Conservative 6; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Klein S., Gerhard D.S.;
Submitted (SFP-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC0802519, AAH82519.1; -.
Hypotherical protein.
SEQUENCE 380 AA; 43570 MW; 8BB938CE776D5238 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel. 28, Created)
(TrEMBLrel. 28, Last sequence update)
(TrEMBLrel. 28, Last annotation update)
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Search completed: October 25, 2005, 15:35:24 Job time : 36.1971 secs
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                                                             Martinez-Duncker I., Oriol R., Mollicone R.;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ781498; CAH03710.1; -.
GO; GO:0016757; Fitransferase activity, transferring glycosyl. . .; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . .; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 SWDLAGYLLYXPXMGRFGNOADHFLGSLAFAKLXVRTLAVPPWIEYQHHKPPFTNLH 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GDP-fucose protein O-fucosyltransferase 1 (EC 2.4.1.221).
GDP-fucose protein O-fucosyltransferase 1 (EC 2.4.1.221).
Name=pofut1; Synonyms=fut12;
Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
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                                                                                                                                                                                                                                                                                                    37 WDSSGYILYCPCMGRFGNQADHFLGSLAFAKNVNRTLVVPPWIVYNHRRPYTNVH 92
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Iferradontoidea; Tetraodontidae; Takifugu.
NCBI_TaxID=31033;
                                                                                                                                                                                                                                                                              6 WDLAGYLLYXPXMGRFGNQADHFLGSLAFAKLXVRTLAVPPWIEYQHHKPPFTNLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (UUL-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ579536; CAE18459.1; -.
ZFIN; ZDB-GENE-040303-2; pofutl.
GO; GO:0046927; F:peptide-O-fucosyltransferase activity; IEA.
GO; GO:0016757; F:transferase activity, transferring glycosyltransferase; Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
Martinez-Duncker I., Mollicone R., Candelier J.J., Breton C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76.4%; Score 249; DB 2; Length 395; larity 75.4%; Pred. No. 7.9e-25; Conservative 5; Mismatches 9; Indels
                                                                                                                                                                                                              Length 396;
                                                                                                                                                                                                           Query Match 76.7%; Score 250; DB 2; Length 39 Best Local Similarity 75.0%; Pred. No. 5.8e-25; Matches 42; Conservative 6; Mismatches 8; Indels
                                                                                                                              Interpro; IPR000886; ER target S.
PROSTIE; PS00014; ER TARGET; UNKNOWN I.
Glycosyltransferase; Transferase Transferase SEQUENCE 396 AA; 45056 WW; F90504E19507073F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  395 AA; 45165 MW; 15BBE06172542E8A CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                  395 AA.
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   Xenopodinae; Xenopus
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Best Local Similarity
Matches 43; Conserv
                                                   SEQUENCE FROM N.A.
               NCBI_TaxID=8364;
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Q7T028
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                                                                                                                                                                                                                                                                                                                                                                                                                        6 WDLAGYLLYXPXMGRFGNQADHFLGSLAFAKLXVRTLAVPPWIEYQHHKPPFTNLH 61
                            Martinez-Duncker I., Mollicone R., Candelier J.J., Oriol R.;
Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ606070; CAES4305.1; -.
GO; GO:0016777; F:transferase activity, transferring glycosyl.
InterPro; IPR000886; ER target S.
PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
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د:
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                      ., Mollicone R., Candelier J.J., Oriol ) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                            Glycosyltransferase, Transferase.
SEQUENCE 384 AA; 43650 MW; 7CAA6ADC90F40032 CRC64;
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Matches 43; Conservative
SEQUENCE FROM N.A.
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against ANA

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Mus muscu Mus muscu Mus muscu AGENCOURT

AGENCOURT

BB631131 BB611933

BB642654

DKFZp459B 170005999

BY752497 B BY752497 B BY752497 B BY7524954 B BY75254 B BY75254 B BY7754 B BY7755 B BY7755 B BY7755 B BY7755 B BY7755 B BY7755 B BY7755 B BY7755 B BY7755 B BY7755 B BY7755 B BY7755 B BY7755 B BY7755 B

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BB631131 BB64264 BB642654 BB642654 BB6778337 BB6778337 BB6778337 BB6787324 CX64629 CX64629 CX64622 CX6462

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602453575 602578756 603052202 601900828

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7968 Full

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Mon		13	305	93.6
		14	305	93.6
OM protein - nucleic s	OM profein - nucleic search, using frame plus b2n model	15	305	93.6
		16	305	93.6
Run on: Octobe	October 26, 2005, 05:59:38 ; Search time 1065.43 Seconds	17	305	93.6
	(without alignments)	18	305	93.6
	2179.320 Million cell updates/sec	19	305	93.6
		20	305	93.6
Title. US-09-	IIS-09-774-954-3	21	305	93.6
t acore:		22	302	95.6
	1 RLAGSWDLAGYLLYXPXMGRLAVPPWIEYQHHKPPFTNLH 61	23	302	95.6
		24	298	91.4
Scoring table: BLOSUM62	962	25	295	90.5
	Xgapon 10.0 . Xgapext 0.5	26	295	90.5
Todack	Yoanext	27	295	90.5
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41111		30	295	90.5
Searched: 342395	14019544 segs. 19032134700 residues	31	295	90.5
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Total number of hits s	The satisfying chosen parameters: 68479088	33	295	90.5
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		41	295	90.5
Command line parameters:	ra.	42	295	90.5
-MODEL=frame+ n2n.mode	el -DBV=xlh	43	295	90.5
-0=/can2 1/USPTO spool	1 h/US09774954/runat 25102005 105432 6406/app query.fasta_1.917	44	295	90.5
-DB=EST -QFMT=fastap	-DB-EST -QFMT-fastap -SUPFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0	45	295	90.2

ALIGNMENTS

RESULT 1

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-Q=/cgn2_1/UGFPTO_expool_h/US09774954/runat_25102005_105432_6406/app_query.fasta_1.917
-D626721_0570_expool_h/US09774954/runat_25102005_10_-LOOPEXT=0
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-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-UNITS=bits -START=1 -END=-1 -MATRIX=D10 -TRANS=human40.cdi -LIST=45
-UNITS=bits -START=1 -END=-1 - THR MIND -MAXIEN=200000000
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-DSQ TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPEXT=0.5 -FGAPEXT=0.5 -FGAPEXT=7 -YGAPEXT=0.5 -DELEXT=7

full-leng 601869779

BE260030 6 CR617950 f BF206548 6

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BU155142 A CO774833 I BI199190 6

		ON BY778150 RIKEN full-length enriched, 17.5 days embryo whole body Mus musculus cDNA clone L930123D17 5', mRNA sequence.		BY778150.1 GI:39704789	EST.	Mus musculus (house mouse)		Eukaryota; Metazoa;	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			Sugahara, Y., Saito, R., Osato, N., Fukuda, S., Sato, K., Watahiki, A.,	Hirozane-Kishikawa,T., Nakamura,M., Shibata,Y., Yasunishi,A.,	Kikuchi, N., Yoshiki, A., Kusakabe, M., Gustincich, S., Beisel, K.,	Pavan, W., Aidinis, V., Nakagawara, A., Held, W.A., Iwata, H., Kono, T.,	Nakauchi, H., Lyons, P., Wells, C., Hume, D.A., Fagiolini, M.,	Hensch, T.K., Brinkmeier, M., Camper, S., Hirota, J., Mombaerts, P.,	Muramatsu, M., Okazaki, Y., Kawai, J. and Hayashizaki, Y.	Targeting a complex transcriptome: the construction of the mouse	full-length cDNA encyclopedia				Contact: Yoshihide Hayashizaki	Laboratory for Genome Exploration Research Group, RIKEN Genomic	Sciences Center(GSC), Yokohama Institute	The Institute of Physical and Chemical Research (RIKEN)	1-7-22 Suehiro-cho, Tsurumi-ku, Yokonama, Kanagawa 230-0045, Japan	
BY778150	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM			REFERENCE	AUTHORS								TITLE		JOURNAL	MEDLINE	PUBMED	COMMENT					

gb_est2. gb_est4... gb_est5... gb_est6... gb_gs81...

est1:* đ EST:*

Jatabase :

		cion				2 BY328132	8 BB633858	0 BB851550	5 B0620C09-	5 BB618795	8 BY728018	5 BB623905
		Description		77815	117534	BY328132	363385	BB851550	715503	B618795	X728018	3B623905
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Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

E l (bases 1 to 33)

Okazaki,Y.; Furuno,M.; Kasukawa,T.; Adachi,J.; Bono,H.; Kondo,S.;

Nikaldo,I.; Osato,N.; Saito,R.; Suzuki,H.; Yamanaka,I.;

Nikaldo,I.; Osato,N.; Saito,R.; Suzuki,H.; Yamanaka,I.;

Kiyosawa,H.; Yagi,K.; Tomaru,Y.; Hasegawa,Y.; Nogami,A.;

Schonbach,C.; Gojobori,T.; Baldarelli,R.; Hill,D.F.; Bult,C.;

Hume,D.A.; Quackenbush,J.; Schriml,L.M.; Kanapin,A.; Matsuda,H.;

Batalov,S.; Beisel,K.W.; Blake,J.A.; Mardio,D.; Brusic,V.;

Chothia,C.; Corbani,L.E.; Cousins,S.; Dalla,B.; Dragani,T.A.;

Fletcher,C.F.; Forrest,A.; Frazer,K.S.; Gaasterland,T.;

Gariboldi,M.; Gassi,C.; Godzik,A.; Gough,J.; Grimond,S.;

Gustinoich,S.; Hirokawa,N.; Jackson,I.J.; Grimond,S.;

Kawaji,H.; Kawasawa,Y.; Kedzierski,R.M.; King,B.L.; Konagaya,A.;
                                                                                                                                                                 Location/Qualifiers

1. .318
| /organism="Mus musculus"
| /organism="Mus musculus"
| /organism="Mus musculus"
| /organism="CSPBL/6"
| /or xefs=taxon:10090"
| /clone="L93012317"
| /tissue_type="Whole body"
| /clone=lib="RIKEN full-length enriched, 17.5 days embryowhole body"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EST 10-DEC-2002
            Email: genome-reseasc.riken.jp, URL:http://genome.gsc.riken.jp/
CDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site (http://genome.gsc.riken.jp/) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   115 CGCTCAGCGGGCTCCTGGGACCTGGCTGCTTCTACTGTCCCTGCATGGGGGCGC 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 PheGlyAsnGlnAlaAspHisPheLeuGlySerLeuAlaPheAlaLysLeu***ValArg 40
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BY175344.1 GI:26311990
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Pax: 81-45-503-9216
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12 (bases 1 to 352)
13 (bases 1 to 352)
14 (bases 1 to 352)
15 (bases)
16 (base)
17 (basto,N., Saito,R., Suzuki,H., Yamanaka,I.,
18 (bytoswa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
18 (schonbach,C., Golobori,T., Baldarelli,R., Hill,D.P., Bult,C.,
18 (bathori,D.A., Quackerbubsh,J., Schrimi,L.M., Kanapin,A., Matsuda,H.,
18 (bathorich,S., Hirokawa,R.) Jake,J.A., Bradt,D., Brusic,V.,
18 (bathorich,S., Hirokawa,N., Jackson,I.J., Jarvis,B.D., Kanai,A.,
18 (bathorich,S., Hirokawa,N., Jackson,I.J., Jarvis,B.D., Kanagani,T.A.,
18 (bathorich,S., Hirokawa,N., Jackson,I.J., Jarvis,B.D., Kanagani,A.,
18 (basi,C., Godzik,A., Gough,J., Grimmond,S.,
18 (basi,C., Godzik,A., Gough,J., Grimmond,S.,
18 (basi,C., Baraterski,R.M., King,B.L., Konagaya,A.,
18 (basi,C., Marchionni,L., McKenaite,L., Marchionni,L., McKenaite,L., Marchionni,L., McKenaite,L., Marchionni,L., McKenaite,L., Marchionni,L., McKenaite,L., Marchionni,R., Perrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S.,
18 (barasi,T., Rechola,Y., Taylor,M.S., Teasdale,R.D., Tanda,M.,
19 (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band) (band
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Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      211 ACCTTGGCTGTACCTCCATGGATTGAATACCAACATCACAAGGCCTCCTTTCACCAACCTC 270
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                  1 ArgLeuAlaGlySerTrpAspLeuAlaGlyTyrLeuLeuTyr***Pro***MetGlyArg
                                                                                                                                                                                                                                                                                                                                                         21 PheGlyAsnGlnAlaAspHisPheLeuGlySerLeuAlaPheAlaLysLeu***ValArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41 ThrLeuAlaValProProTrpIleGluTyrGlnHisHisLysProProPheThrAsnLeu
Mismatches:
Indels:
                                                                           Gaps:
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   Best Local Similarity:
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PUBMED
COMMENT
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ACCESSION VERSION KEYWORDS SOURCE

RESULT 3 BY328132

REFERENCE AUTHORS JOURNAL

TITLE

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rax: a.1-3-3-12-12

Raxial: genome-res@gec.riken.jp, URL:http://genome.gec.riken.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
Hirozana,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,
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CDNA library was prepared and sequence din Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in Riken
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BB633858
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Tissues were provided by Vassilis Aidinis ( Biomedical Sciences Tissues were provided by Vassilis Aidinis ( Immunology 14-16 Al. Research Center 'Al. Fleming' Institute of Immunology 14-16 Al. Fleming street 16672 Vari, Greece ) whose assistance we gratefully acknowledge.
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further details.
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/clone lib="RIKEN full-length enriched, synovial
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/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="L130001N19"
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91.80%
91.80%
93.56%
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ORGANISM

VERSION KEYWORDS SOURCE

REFERENCE AUTHORS

TITLE JOURNAL COMMENT

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Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
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Tel: 81-45-503-9216
Email: genome-resegec.riken.jp, URL:http://genome.ggc.riken.jp/
Carninci, P., Shibata, Y., Hayafsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare Genome Res. . 10 (10), 167-1630 (2000)
genes. Genome Res. . 10 (10), 167-1630 (2000)
wagi, K., Pujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,
Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T.,
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B. 1 (bases 1 to 480).

B. Akimura,T., Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T., Hayatau,N., Hiranoto,K., Hiraoka,T., Hirotani,K., Indtani,K., Ito,M., Kawai,J., Kojima,Y., Konno,H., Konda,M., Matsuyama,T., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Okada,T., Saito,K., Sakai,K., Sakazui,R., Sakazki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Tomaru,A., Toyar,T., Watahiki,A., Takaku-Akahira,S., Muramatsu,M. and Hayashiati,Y., Watahiki,A., Yasunishi,A., Muramatsu,M. and Hayashiati,Y.
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BB851550 G1:17093004
21 PheGlyAsnGlnAlaAspHisPheLeuGlySerLeuAlaPheAlaLysLeu***ValArg
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Matches:
Conservative:
Mismatches:
Indels:
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The Institute of Physical and Chemical Research (RIKEN)
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Teurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9212
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                                                                                                                                                                                                                                                                                         Arakawar, Carrinci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hori, F., Ishi, Y., Ito, M., Kawai, J., Konao, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Salto, R., Saki, R., Sanaki, Y., Okido, T., Salto, R., Saki, T., Sanaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y. RIKEN Mouse ESTB (Arakawa, T., et al. 2001)
Unpublished (2001)
                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

    .456
    /organism="Mus musculus"
/mol_type="mRNA"
    /db_xref="taxon:10090"

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Piao, Y., Ko, N.T., Lim, M.K. and Ko, M.S.H.
Construction of long-transcript enriched cDNA libraries from submicrogram amounts of total RNAs by a universal PCR amplification method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Stono, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:10090"
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/cell_type="B16 Fl0% cells"
/clone_lib="RIKEN full-length enriched, B16 Fl0% cells"
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Laboratory of Genetics
National Institute on Aging/National Institutes of Health
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                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
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s'-pdACTAGTTCAGATCGCGGCCCCCTTTTTTTTTTTTTTTT-3'] from 0.2 ug of total RNA, treated with T4 DNA polymerase, and 0.2 ug of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The CDNAs were ligated to Lone-linker LL-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the CDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-5. The products were purified by phenol/chloroform and Centricon 100. The CDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pSPORTI plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method: The average insert size is about 2.2 kb. The library was constructed by Yulan Piao (NIA)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue type="Blastocyst"
/dev_stage="3.5-dpc"
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/lab.host="Blublob"
/clone lib="NiA Mouse Blastocyst cDNA Library (Long)"
/clone lib="NIA Mouse Blastocyst cDNA Library (Long)"
/clone lib="NIA Mouse Blastocyst cDNA Librarory of Genetics,
NotE; Mouse CDNA project by the Laboratory of Genetics,
NotE; Mouse CDNA project by the Laboratory of Genetics,
NotE; Mouse CDNA Project by the Laboratory of Genetics,
NotE; Mouse CDNA Project by the Laboratory of Genetics,
NotE; Mouse CDNA Library (Ref. Genome Res.
11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were
extracted from a pool of 20 Blastocysts. Double-stranded
CDNAS were synthesized with an Oligo(dT) primer
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DEFINITION BB618795 RIKEN full-length enriched, 8 days embryo Mus musculus
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                                                     Email: cdna@lgsun.grc.nia.nih.gov
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High quality sequence stop: 536
POLYA=No.
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/mol_type="mRNA"
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Best Local Similarity:
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AL Unpublished (2001)
Contact: Yoshihde Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute of RESPICATION CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONTESTIVE CONT
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Mus musculus (house mouse)

Mus musculus (hotata; Craniata; Vertebrata; Buteleostomi; Butaryota; Metazoa; Chordata; Ciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 604)

Arakawa, T., Carninoi, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishi, Y., Ito, M., Kawai, J., Sonno, H., Korda, M., Koya, S., Matsuyama, T., Miyazaki, J., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sanaki, Y., Sabaki, T., Sabaki, T., Sabaki, T., Sabaki, T., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y. RIKEN Mouse ESTS (Arakawa, T., et al. 2001)
cDNA clone 5730432G02 5', mRNA sequence.
BB618795
BB618795.1 GI:15396691
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Amol_type="mRNA"
Firtain="C57BL/6"
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/clone="5730432G02"
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By Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazaa; Chordata; Craniata; Vartebrata; Euteleostom;

Eukaryota; Metazaa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

Chases I to 603)

Sciurognathi; Muridae; Musinae; Mus.

Kiyosawa, H., Yaqi, K., Toatu, Y., Hasegawa, Y., Nogami, A., Rivado, I., Costo, N., Saito, R., Sizuki, H., Yamanaka, I., Kondo, S., Kiyosawa, H., Yaqi, K., Toatu, Y., Hasegawa, Y., Nogami, A., Butado, I., Costo, M., Entrimi, L.M., Kanapin, A., Mutsuda, H., Batalov, S., Beisel, K.W., Frazer, K.S., Gaasterland, T., Corbani, L.E., Cousins, S., Dalia, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Garibold, M., Gissl, K.W., King, B.L., Konagani, T.A., Kawali, H., Kawasawa, Y., Cordani, C., Godzik, A., Garimond, S., Ravali, T.V., Lee, Y., Lenhard, B., L., Magashima, T., Kurchkin, I.V., Lee, Y., Lenhard, B., L., Magashima, T., Muteis, L., Marchionni, L., Morkenzie, L., Miki, H., Magashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Peocle, G., Pertea, G., Peocle, G., Pertea, G., Peocle, G., Sendelin, R., Schneidder, C., Sendle, J.U., Ol, D., Ramachandran, S., Sandelin, R., Schneidder, C., Sendle, J. Wang, T., Konn, M., Yang, I., Vang, I., Wang, L., Wang, K., Mang, 728018 RIKEN full-length enriched, 10 days neonate cerebellum Mus musculus cDNA clone B930076G19 5', mRNA sequence.
BY728018
BY728018.1 GI:27141145
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Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
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Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
                                                                                                                                                                                                                        1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
Fax: 81-45-503-9216
Rogers, J., Birney, E. and Hayashizaki, Y.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
                                                                                                                                                                                                                                                                                           Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P.,
Fukuda,S., Hashizume, W., Hayashida,K., Hirozane,T., Hori,F.,
Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y.,
Rondo,S., Konno,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M.,
Nomura,K., Numazaki,R., Ohno,M., Ohasto,N., Salto,R., Sakazume,N.,
Sano,H., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M.,
Direct Submission
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Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
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Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
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/dev_stage="10 days neonate"
/lab_host="DH108"
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/strain="C57BL/6J"
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FEATURES

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BB623905 RIKEN full-length enriched, adult male adrenal gland Mus musculus cDNA clone 7330430107 5', mRNA sequence.
BB623905
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases I to 611)
Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T.,
Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J.,
Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K.,
Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K.,
Sano, H., Saaski, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F.,
Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.
Unpublished (2001)
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Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
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Carninoi,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected CDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Pujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Matsuira,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A.
and Hayashizaki,Y.
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Genome Res. 10 (11), 1757-1771 (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (
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                                                   305.00
91.80%
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                                                                                                 Percent Similarity:
Best Local Similarity:
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COMMENT
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                                                                                                                                                                                                                            BY752500 614 bp mRNA linear EST 17-DEC-2002 BY752500 RIKEN full-length enriched, 9.5 days embryo parthenogenote Mus musculus cDNA clone B130006A17 5', mRNA sequence.
                                                                                                                                                                    117 CGGTCAGCGGGCTCCTGGGACCTGGCCGGTTACCTGTCTTACTGTCCTGCATGGGGCGC 176
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Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Alizawa,K., Eukuda,S., Hara,A., Itch,M., Kawai,J., Shibata,K. and Hayashizaki,Y.
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Flease visit our web site (http://genome.gsc.riken.go.jp) for further details.
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                         /organism="Mus musculus"
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SMAR meneculas (House mouse)

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10. Morakaki, Y. Pruno, M. Kashto, R., Sarkoki, H., Yamanaka, I., Morakaki, Y. Pruno, M. Saikok, R., Sarkoki, H., Yamanaka, I., Schonbah, C., Godobri, T., Baldarelli, R., Hilli, D. P., Bult, C., Schonbah, R., Osato, M., Manamaka, M., Schonbah, C., Godori, T., Baldarelli, R., Milli, D. P., Bult, C., Godori, T., Baldarelli, R., Milli, D. P., Bult, C., Godori, T., Baldarelli, R., Milli, D. P., Bult, C., Godori, T., Schonbah, R., Manamilas M., Schonbah, C., Corpentia, C., Corpentia, C., Corpentia, C., Godorik, R., Manamila, R., Manami, M., Chiesi, C., Godorik, R., Manami, S., Manami, M., Sahom, M., Manami, M., Sahom, M., Sahom, M., Sahom, M., Sahom, M., Sahom, M., Sahom, M., Sahom, M., Sahom, M., Sahom, M., Sahom, M., Sahom, M., Sahom, M., Sahom, M., Sahom, M., Sahom, M., Sahom, M., Sahom, M., Sahom, M., Sahom, M., Sahom, M., Sahom, M., Sahom, M., Sahom, M., Sahom, M., Sahom, M., Sahom, M., Sahom, M., Sahom, M., Sahom, M., Sahom, M., Sahom, M., Sahom, M., Sahom, M., Sahom, M., Sahom, M., Sahom, M., Sahom, M., Sahom, M., Sahom, M., Sahom, M., Sahom, M., Sahom, M., Sahom, M., Sahom, M., Sahom, M., Sahom, M., Sahom, M., Sahom, M., Sahom, M., Sahom, M., Sahom, M., Sahom, M., Sahom, M., Sahom, M., Sahom, M., Sahom, M., Sahom, M., Sahom, M., Sahom, M., Sahom, M., Sahom, M., Sahom, M., Sahom, M., Sahom, M., Sahom, M., Sahom, M., Sahom, M., Sahom, M., Sahom, M., Sahom, M., Sahom, M., Sahom, M., Sahom, M., Sahom, M., Sahom, M., Sahom, M., Sahom, M., Sahom, M., Sahom, M., Saho
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Tel: 81-45-503-9222
Fax: 81-45-503-9216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of subtraction to Rot = 229.0 Second strand cDNA was prepared with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EST 26-OCT-2001
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 634)
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                                                                                                                                                                                                                                                                                         Inote="Site 1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in
                                                                                                                                                                                                                                                                                                                                                                          RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                      /clone_lib="RIKEN full-length enriched, 9.5 days embryo
parthenogenote"
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                                    Please visit our web site (http://genome.gsc.riken.go.jp) further details.
Kanagawa Prefecture, Japan) whose assistance we gratefully
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Matches:
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Mismatches:
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                                                                                                                                                                                        /tissue_type="parthenogenote"
/dev_stage="9.5 days embryo"
/lab_host="DH108"
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                                                                                                                                     'mol_type="mRNA"
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RIKEN integrated sequence analysis (RISA) system--384-format RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Alzawa, K., Pukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and Hayashizaki, Y.
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
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                                                                                                                                                                                                                                                                                                           Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Teurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: genome-reseges riken.jp, URL:http://genome.ges.riken.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
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genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Matahiki,M., Yoneda,Y., Ishikawa,I., Muramatsu,M., Inoue,Y., Kira,A.
and Hayashizaki,Y.
Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J.,
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Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.
RIKEN Mouse ESIR (Arakawa, T., et al. 2001)
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650 bp mRNA linear EST 17-DEC-2002 BY752497 RIKEN full-length enriched, 9.5 days embryo parthenogenote Mus musculus cDNA clone B130001118 5', mRNA sequence.
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Hayashizaki,Y. Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                          clone lib="RIKEN full-length enriched, 15 days embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ArgleuAlaGlySerTrpAspLeuAlaGlyTyrLeuLeuTyr***Pro***MetGlyArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 PheGlyAsnGlnAlaAspHisPheLeuGlySerLeuAlaPheAlaLysLeu***ValArg
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                              e mouse tissues.
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BY752497.1 GI:27183400
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Wans muscotius

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 641)

8 Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T.,

8 Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T.,

Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K.,

Konno,H., Koda,M., Koya,S., Mistayama,T., Miyazaki,C., Sakai,K.,

Sagab,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F.,

Sogabo,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F.,

RIKEN Mouse ESTE (Arakawa,T., et al. 2001)

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Fax: 81-45-503-922

Ratill-length ond subtraction of cap-trapper-selected conNa to prepare full-length cDNA libraries for rappid discovery of new genee. Genome Res. 10 (10), 1617-1630 (2000)

Wagi,K., Fuliwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,B.,

Matchiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T.,

Matchiki,M., Yoneda,Y., Ishikawa,Y., Togawa,Y., Tawa,M., Ohara,B.,

Matchiki,M., Yoneda,Y., Ishikawa,Y., Togawa,X., Tanaka,T.,

Matchiki,M., Yoneda,Y., Shibata,K., Itch,M., Carninci,P.,

RIKEN integrated sequence analysis (RISA) system-38-format Res.

10 (11), 1757-1771 (2000)

Konno,H., Fukunishi,Y., Shibata,K., Itch,M., Carninci,P.,

Sugahara,Y. and Hayashizaki,Y.

Computer-based methods for the mouse full-length CDNA

Computer-based methods for the mouse full-length CDNA

Computer-based methods for the mouse full-length Construction of a norecludant CDNA library. Genome Res. 11 (10), Shibata,K., Rhibata,K., Rhibawa,K., Rhibata,K., Rhibawa,K., Takawa,K., Shibata,K., and Alzawa,K., Tukuda,S., Kara, Takawa,K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BB611933 RIKEN full-length enriched, 15 days embryo head Mus musculus cDNA clone 4021401D01 5', mRNA sequence.
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                                                                                                                                                                                                                                                         21 PheGlyAsnGlnAlaAspHisPheLeuGlySerLeuAlaPheAlaLysLeu***ValArg
                                                                                                                                                                                                                                                                                                                                            41 ThrLeuAlaValProProTrpIleGluTyrGlnHisHisLysProProPheThrAsnLeu
    0 0 0
  Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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BB611933.1 GI:16453020
                       Similarity:
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                  Percent Simil
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DB:
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BB611933
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location/Qualifiers

FEATURES

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mamaalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinamalia; Butheria; Rodentia; Sciurognathi; Murinae; Musinamalia; Eutheria; Rodentia; Sciurognathi; Murinae; Musinabata; I. Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojoboti, T., Baldarelli, R., Hill, D.P., Bult, C., Schonbach, C., Corbani, L.E., Cousins S., Dalla, E., Dragani, T.A., Batchor, C., Corbani, L.E., Cousins S., Dalla, E., Dragani, T.A., Gariboldi, M., Gisel, C., Godali, R., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gisel, C., Godali, C., Godali, E., Dragapi, T.A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B. L., Konagaya, A., Kawaji, H., Kawasawa, Y., Lee, Y., Lenhard, B., Lyons, P.M., Maglott, D.R., Murcchkin, T.V., Lee, Y., Lehhard, B., Lyons, P.M., Maglott, D.R., Mattaig, L., Marchonni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W. J., Perta, G., Pescole, G., Ravasi, T., Redi, J.C., Red, D.J., Reid, J. V., Qi, D., Ramachandran, S., Shitana, R., Schneider, C., Sendle, C., Setou, M., Shimada, K., Sandelin, A., Schneider, C., Sendle, C., Mang, Y., Warande, M., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hilmig, L.G., Wymhaw Boris, A., Yangisawa, M., Yang, L., Washawa, T., Kohno, H., Wakal, J., A., Sakai, M., Saraki, D., Shibata, K., Indays, S., Shibata, K., Indays, S., Shibata, K., Indays, S., Shibata, K., Indays, S., Shibaga, A., Shibagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y., Wasaki, D., Shibata, K., Shibata, S., ```

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Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P.,
Fukuda,S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F.,
Imotani,K., Ishi,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y.,
Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Saito,R., Sakazume,N.,
Sano,H., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M.,
Takeda,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y.
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COMMENT

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Direct Submission
Computerational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Namm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraties for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA
computer-based methods for the mouse full-length cDNA
computer-based methods for the mouse full-length cDNA
computer-based methods for the mouse full-length cDNA
computer-based methods for the mouse full-length cDNA
computer-based methods for the mouse full-length cDNA
construction of sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome
Genomic Sciences Center and Genome Styloration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Tissues were provided by Dr. Tomohiro Kono (Department of Animal
Science, Tokyo University of Agriculture, 1737 Hunako Atsugi City,
Kanagawa Prefecture, Japan) whose assistance we gratefully
```

Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

acknowledge.

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/note="Site" 1: Sall; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5, GAGGAGAGARCAAGAGCTCTTTTTTTTTTTTTTTV 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of subtraction to Rot = 229.0 Second strand cDNA was prepared with the
 BB642654 BIKEN full-length enriched, adult retina Mus musculus CDNA
 1 (bases 1 to 661)
Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T.,
Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J.,
Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K.,
Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K.,
Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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0
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 Mus musculus (house mouse)
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305.00
91.80%
91.80%
 Mus musculus
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 61 His 61
 Percent Similarity:
 Alignment Scores:
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Mismatches: Indels: Gaps:

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BY728337.1 GI:27141464
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93.56%
Best Local Similarity:
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 Unpublished (2001)
Loboratory Conteact: Yoshinide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
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 Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Kakeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y. RIKEN Mouse ESTS (Arakawa, T., et al. 2001)
Unpublished (2001)
 Location/Qualifiers
Location/Qualifiers
1. 661
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 e mouse tissues.
 FEATURES
 ORIGIN
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Length: Matches: Conservative:

2.33e-31 305.00 91.80%

Alignment Scores: Pred. No.: Score: Percent Similarity:

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BY728337 RIKEN full-length enriched, 16 days embryo head Mus
musculus cDNA clone C130003G23 5', mRNA sequence.
 Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
 178 TTTGGGAACCAGGCTGATCACTTCTTGGGCTCCCTGGCATTTGCGAAGCTGCTGAACCGC 237
 40
 41 ThrLeuAlaValProProTrpIleGluTyrGlnHisHisLysProProPheThrAsnLeu 60
21 PheGlyAsnGlnAlaAspHisPheLeuGlySerLeuAlaPheAlaLysLeu***ValArg
 Mus musculus (house mouse)
Mus musculus
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Direct Summission.

Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 157-171 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Genomic Sciences Center and Genome Science in Riken contributed to
 Email: genome-resegge.riken.jp, URL.http://genome.gsc.riken.jp/
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P.,
Fukuda,S., Hashizume,W., Hayashida,K., Hirozane,T., Hort,F.,
Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y.,
Kondo,S., Konno,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M.,
Nomura,K., Numazaki,R., Ohno,M., Ohaato,N., Saito,R., Sakazume,N.,
Zasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M.,
Direct Submission
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US-09-774-954-3 (1-61) x BY728337 (1-664)

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Length:
Matches:
Conservative:
Mismatches:

2.34e-31 305.00 91.80% 91.80%

Percent Similarity: Best Local Similarity:

Query Match: DB:

Alignment Scores: Pred. No.:

ORIGIN

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 Search completed: October 26, 2005, 15:17:23 Job time: 1076.43 secs
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 61 His 61
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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

- nucleic search, using frame\_plus\_p2n model OM protein October 26, 2005, 09:31:14 ; Search time 260.659 Seconds (without alignments) 1931.299 Million cell updates/sec Run on:

US-09-774-954-3 326 Title: Perfect score:

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**BLOSUM62** Scoring table:

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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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| 33 66.5 20.4 2162598 22 US-10-472-928-4979 Sequence 4979, 34 66 20.2 361 13 US-00-925-065A-476650 Sequence 47650, 36 20.2 361 13 US-00-925-065A-476650 Sequence 47650, 36 19.9 478 19 US-10-152-319A-21 Sequence 47650, 37 65 19.9 1437 19 US-10-437-963-80416 Sequence 80416, 37 65 19.9 2910 19 US-10-424-599-40441 Sequence 40431, 39 65 19.9 513509 10 US-10-424-599-40437 Sequence 40431, 41 64.5 19.8 476 13 US-09-754-065A-500789 Sequence 500787, 42 64.5 19.8 628 13 US-10-511-467-1068 Sequence 500788, 43 64.5 19.8 628 13 US-09-925-065A-770388 Sequence 770388, 44 64 19.6 10.0 24 US-10-972-079-32895 Sequence 36872.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 32    | w    | ٠.    | 86     | 18 | 0-158-844-113      | equence 113, Ap |
| 34         66         20.2         361         13         US-09-925-065A-476650         Sequence 47665           35         65         19.9         478         19         10-10-152-319A-21         Sequence 40.17           37         65         19.9         1437         19         US-10-424-599-40441         Sequence 40431           38         65         19.9         1437         19         US-10-424-599-40437         Sequence 40431           40         64.5         19.9         513509         10         US-09-754-853A-4         Sequence 50078           41         64.5         19.8         476         13         US-09-925-065A-50078         Sequence 50078           41         64.5         19.8         476         13         US-09-925-065A-50078         Sequence 50078           42         64.5         19.8         476         13         US-09-925-065A-50078         Sequence 50078           43         64.5         19.8         628         13         US-10-631-467-1068         Sequence 7703           44         64.5         19.6         600         24         US-10-925-065A-70388         Sequence 7703           45         19.6         10.10         11         US-10-9-325-0                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 33    | w    |       | 216259 | ~  | US-10-472-928-497  | 4979            |
| 35 65 19.9 478 19 US-10-152-319A-21 Sequence 21, R 36 19.9 519 20 US-10-424-599-4041 Sequence 80416 Sequence 80416 Sequence 80416 Sequence 80416 Sequence 40441 38 65 19.9 2910 19 US-10-424-599-40441 Sequence 404431 39 65 19.9 513509 10 US-09-754-853A-4 Sequence 404431 Sequence 50077 41 64.5 19.8 476 13 US-09-925-065A-50078 Sequence 50077 42 64.5 19.8 575 24 US-10-631-467-1068 Sequence 50077 43 64.5 19.8 628 13 US-09-925-065A-500788 Sequence 50077 44 64 19.6 600 24 US-10-212-2079-32895 Sequence 77038 Sequence 36072 44 64 19.6 600 24 US-10-212-2079-32895 Sequence 36072 45 19.8 628 13 US-09-925-065A-770388 Sequence 37038 44 64 19.6 600 24 US-10-212-2079-32895 Sequence 376975 Sequence 376975 Sequence 376975 Sequence 376975 Sequence 376975 Sequence 376975 Sequence 376975 Sequence 376975 Sequence 376975 Sequence 376975 Sequence 376975 Sequence 376975 Sequence 376975 Sequence 376975 Sequence 376975 Sequence 376975 Sequence 376975 Sequence 376975 Sequence 376975 Sequence 376975 Sequence 376975 Sequence 376975 Sequence 376975 Sequence 376975 Sequence 376975 Sequence 376975 Sequence 376975 Sequence 376975 Sequence 376975 Sequence 376975 Sequence 376975 Sequence 376975 Sequence 376975 Sequence 376975 Sequence 376975 Sequence 376975 Sequence 376975 Sequence 376975 Sequence 376975 Sequence 376975 Sequence 376975 Sequence 376975 Sequence 376975 Sequence 376975 Sequence 376975 Sequence 376975 Sequence 376975 Sequence 376975 Sequence 376975 Sequence 376975 Sequence 376975 Sequence 376975 Sequence 376975 Sequence 376975 Sequence 376975 Sequence 376975 Sequence 376975 Sequence 376975 Sequence 376975 Sequence 376975 Sequence 376975 Sequence 376975 Sequence 376975 Sequence 376975 Sequence 376975 Sequence 376975 Sequence 376975 Sequence 376975 Sequence 376975 Sequence 376975 Sequence 376975 Sequence 376975 Sequence 376975 Sequence 376975 Sequence 376975 Sequence 376975 Sequence 376975 Sequence 376975 Sequence 376975 Sequence 376975 Sequence 376975 Sequence 376975 Sequence 376975 Sequence 376975 Sequence 376975 Sequence 376975 Seque | 34    | 99   |       | ٣      | 13 | -09-925-065A-47665 | 47665           |
| 36 65 19.9 519 20 US-10-437-963-80416 Sequence 80418 37 65 19.9 1437 19 US-10-424-599-40441 Sequence 40441 38 65 19.9 2910 US-10-424-599-40437 Sequence 4 00441 39 65 19.9 513509 10 US-09-754-853A-4 40 64.5 19.8 476 13 US-09-925-065A-500787 Sequence 50078 42 64.5 19.8 476 13 US-09-925-065A-500788 Sequence 50078 43 64.5 19.8 628 13 US-10-631-467-1068 Sequence 77038 44 64 19.6 600 24 US-10-631-467-1088 Sequence 77038 45 64.5 19.8 628 13 US-09-925-065A-770388 Sequence 77038                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | m     | 65   |       | 4      | 19 | -10-152-319A-2     | 21, 7           |
| 37 65 19.9 1437 19 US-10-424-599-40441 Sequence 40441<br>38 65 19.9 2910 19 US-10-424-599-40437 Sequence 40431<br>40 64.5 19.8 476 13 US-09-754-853A-4 Sequence 50078<br>41 64.5 19.8 476 13 US-09-925-065A-500788 Sequence 50078<br>43 64.5 19.8 628 13 US-09-925-065A-500788 Sequence 50078<br>44 64 19.6 600 24 US-10-631-467-1068 Sequence 77038<br>45 64.5 19.8 628 13 US-09-925-065A-770388 Sequence 77038<br>46 19.6 600 24 US-10-782-1073-38995 Sequence 36872                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | ייי   | 65   |       | Ŋ      | 20 | -10-437-963-8041   | 80416           |
| 65 19.9 2910 19 US-10-424-599-40437 Sequence 40437<br>64.5 19.9 513509 10 US-09-754-853A-4 Sequence 50078<br>64.5 19.8 476 13 US-09-925-065A-500788 Sequence 50078<br>64.5 19.8 476 13 US-09-925-065A-500788 Sequence 50078<br>64.5 19.8 675 24 US-10-631-467-1068 Sequence 1068,<br>64.5 19.8 628 13 US-09-925-065A-770388 Sequence 1068,<br>64.5 19.8 628 13 US-09-925-065A-770388 Sequence 32895<br>64.5 19.8 600 24 US-10-631-467-1068 Sequence 32895                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | 3.7   | 65   |       | 14     | 19 | -10-424-599-4044   | 4044]           |
| 65 19.9 513509 10 US-09-754-853A-4 Sequence 4, Ag 1 US-09-925-065A-500787 Sequence 50078 Sequence 50078 Sequence 50078 Sequence 50078 Sequence 50078 Sequence 50078 Sequence 50078 Sequence 50078 Sequence 50078 Sequence 50078 Sequence 50078 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequence 70038 Sequenc | 38    | 65   |       | 29     | 19 | -10-424-599-4043   | 40437           |
| 0 64.5 19.8 476 13 US-09-925-065A-500787 Sequence 500787 1 64.5 19.8 476 13 US-09-925-065A-500788 Sequence 500788 2 64.5 19.8 675 24 US-10-631-467-1068 Sequence 1068, 2 64.5 19.8 628 13 US-09-925-065A-770388 Sequence 770388 4 64 19.6 600 24 US-10-972-079-38995 Sequence 38995, 2 64.5 10.18 18 19-10-72-3895                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | 39    | 65   |       | 5135   | 10 | -09-754-853A-4     | e 4, Ag         |
| 1 64.5 19.8 476 13 US-09-925-065A-500788 Sequence 500788 2 64.5 19.8 575 24 US-10-631-467-1068 Sequence 1068, 3 64.5 19.8 628 13 US-09-925-065A-770388 Sequence 770388 4 64 19.6 600 24 US-10-972-079-32895 Sequence 32895, 5 64 19.6 10.18 18 1910-372-37872 Sequence 35895, 5 64 19.6 19.6 10.18 18 1910-372-37872 Sequence 35895, 5 64 19.6 10.18 18 1910-372-37872 Sequence 35895, 5 64 19.6 10.18 18 1910-372-37872 Sequence 35895, 5 64 19.6 10.18 18 1910-372-37872 Sequence 35895, 5 64 19.6 10.18 18 1910-372-37872 Sequence 35895, 5 64 19.6 10.18 18 1910-372-37872 Sequence 35895, 5 64 19.6 19.6 19.6 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | 40    |      |       | 4      | 13 | -09-925-065A-50078 | ence 500        |
| 2 64.5 19.8 575 24 US-10-631-467-1068 Sequence 1068, 3 64.5 19.8 628 13 US-09-925-065A-770388 Sequence 770388 4 64 19.6 600 24 US-10-972-079-32895 Sequence 32895, 5 connence 35895, 5 connence  | 41    |      |       | 4      | 13 | -09-925-065A-50078 | ence 500788     |
| 3 64.5 19.8 628 13 US-09-925-065A-770388 Sequence 770388<br>4 64 19,6 600 24 US-110-972-079-32895 Sequence 32895,<br>5 7 10 10 10 11 11 110-382-16872 Sequence 3895,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | 42    |      |       | S      | 24 | -10-631-467-106    | ence 1068,      |
| 4 64 19.6 600 24 US-10-972-079-32895 Seguence 32895                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 43    |      |       | 9      | 13 | -09-925-065A-77038 | ence 77038      |
| E 64 10 6 1019 18 119-10-282-1228-36872 Seguence 3687                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |       |      |       | •      | 24 | -10-972-079-3289   | ence 32895,     |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |       | 4.4  |       | 70     | 18 | -10-282-122A-368   | equence 3687    |

ALIGNMENTS

RESULT 1
US-09-774-954-16

| Sequence 16, Application US/09774954 |
| Publication No. US20040241645A1 |
| GENERAL INFORMATION: APPLICANT: Yang Wang, Michael W. Spellman TITLE OF INVENTION: O. PROCRYLTANGES: 17 CORRESPONDENCE ADDRESS: CORRESPONDENCE ADDRESS: STREET: 1 DNA WAY |
| STREET: 1 DNA WAY |
| STREET: COUNTRY: USA |
| COUNTRY: USA

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RESULT 3
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 ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: Withpatin (Genentech)
CURRATT APPLICATION DATA:
APPLICATION NUMBER: US/09/774,954
FILING DATE: 30-Jan-2001
CLASSIFICATION NUMBER: US/08/978,741
APPLICATION NUMBER: US/08/978,741
APPLICATION NUMBER: US/08/978,741
APPLICATION NUMBER: US/08/978,741
APPLICATION NUMBER: US/08/978,741
ATTORNEY/AGENT INFORMATION:
NAME: SVODGA, CTAIG G
RECERENCE/DOCKET NUMBER: 39,044
REFERENCE/DOCKET NUMBER: 1941P1
TELECHONE SODGA, CTAIG G
RECERENCE/DOCKET NUMBER: 1941P1
TELECHONE 650/25-1489
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHRACTERISTICS:
LENGTH: 1100 base pairs
TYPE: Nucleic Acid
STRANDENDESS: SING1E
 COUNTRY: USA

COMPUTER: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatibale

COMPUTER: IBM PC compatibale

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinParin (Genentech)
 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
 US-09-774-954-3 (1-61) x US-09-774-954-16 (1-1100)
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295.00
91.53%
90.49%
 Score:
Percent Similarity:
Best Local Similarity:
Query Match:
DB:
 Alignment Scores:
Pred. No.:
 US-09-774-954-16
 RESULT 2
US-09-774-954-4
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THE OF THE REPRENCE OF SECONDARY OF THE REPRENCE OF SECONDARY IN THE OF INVENTION WILLS OF INVENTION: WHITH THE OF INVENTION: WHITH APPLICANT: WHITH WOLLS, WILLIAM TITLE OF INVENTION: WHITH OSTEOARTHRITS AND HUMAN PROTEASES

TITLE OF INVENTION: WHOSTEOALD ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH THE OF INVENTION: WHOSTEOARTHRITS AND HUMAN PROTEASES

TITLE OF INVENTION: WHOSTE: US/10/956,157

CURRENT APPLICATION WHOSER: US/10/956,157

CURRENT FILING DATE: 2004-10-04

NUMBER OF SEQ ID NOS: 319805

SOFTWARE: PARENTE OF SECONDARY OF SECO
 Length:
Matches:
Conservative:
Mismatches:
Indels:
 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
CURRENT APPLICATION DATA:

APPLICATION UNUBER: US/09/774,954
FILING DATE: 30-Jan-2001
CLASSIFCATION: cunknown>
PRIOR APPLICATION BATE: 10-Jan-1907
APPLICATION NUMBER: US/08/978,741
FILING DATE: 26-NOV-1997
ATTORNEY/AGENT INFORMATION:
NAME: SOFOOGA, CTAIG G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: 91,044
REFERENCE/DOCKET NUMBER: 91,044
TELEPHONE: 650/25-1489
INFORMATION FOR SEO, ID NO: 4:
SEQUENCE CHARACTERISTICS:
LEBROTH: 130 Dase pairs
TYPE: NUCLEIC ACID
STRANDEDINESS: SINGLE
STRANDEDINESS: SINGLE
STRANDEDINESS: SINGLE
 US-09-774-954-3 (1-61) x US-09-774-954-4 (1-1300)
 TOPOLOGY: Linear SEQUENCE DESCRIPTION: SEQ ID NO: 4: US-09-774-954-4
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295.00
91.53%
91.53%
 4.42e-33
295.00
91.53%
90.49%
 TYPE: DNA
CORGANISM: Homo sapiens
US-10-956-157-9986
 Percent Similarity: 5
Best Local Similarity: 9
Query Match: 9
DB:
 Percent Similarity:
Best Local Similarity:
Query Match:
 Alignment Scores:
Pred. No.:
 Alignment Scores:
Pred. No.:
```

```
APPLICANT: Guillemette, Tracy L.
APPLICANT: Guillemette, Tracy L.
APPLICANT: Guillemette, Tracy L.
APPLICANT: Guillemette, Tracy L.
APPLICANT: Schlegel, Robert
APPLICANT: Schlegel, Robert
APPLICANT: Schlegel, Robert
APPLICANT: Thibodeau, Stephen N.
APPLICANT: Thibodeau, Stephen N.
APPLICANT: Burgart, Lawrence J.
TITLE OF INVENTION: NETHENDS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, THERAPY OF COLON CANCER
TITLE OF INVENTION: THERAPY OF COLON CANCER
TITLE OF INVENTION: THERAPY OF COLON CANCER
FILE REFERENCE: MPMOI-029P2RNM
CURRENT APPLICATION NUMBER: US/10/301,822
CURRENT PILING DATE: 2002-11-21.
PRIOR PILING DATE: 2001-12-10
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 3 AlaGlySerTrpAspLeuAlaGlyTyrLeuLeuTyr***Pro***MetGlyArgPheGly
 43 AlaValProProTrplleGluTyrGlnHisHisLysProProPheThrAsnLeuHis
 COMPUTER KEALCHAILS TORM:
COMPUTER: 15.5 inch, 1.44 Mb floppy disk
COMPUTER: 15M PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Windatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/774,954
FILING DATE: 30-Jan-2001
CLASSIFICATION: «Unknown-
PRIOR APPLICATION NUMBER: US/08/978,741
FILING DATE: 26-NOV-1997
APPLICATION NUMBER: 08/792,498
FILING DATE: 31-JAN-1997
APPLICATION NUMBER: 08/792,498
FILING DATE: 31-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: 39,044
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
 1514
54
0
5
0
 Conservative:
Mismatches:
Indels:
 US-09-774-954-3 (1-61) x US-09-774-954-1 (1-1514)
 Length:
Matches:
 Sequence 168, Application US/10301822
Publication No. US20030148410A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
 SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 LENGTH: 1514 base pairs
 TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
 TYPE: Nucleic Acid
STRANDEDNESS: Single
 5.27e-33
295.00
91.53%
91.53%
 TOPOLOGY: Linear
 Percent Similarity:
Best Local Similarity:
 US-10-301-822-168
 Alignment Scores:
 US-09-774-954-1
 Query Match:
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 g
 Sequence 4751, Application US/10956157

Suguence 4751, Application US/10956157

Suguence 4751, Application US/10956157

Sublication No. US20050118625A1

GENERAL INFORMATION:
APPLICANT: Wyelh
APPLICANT: Wounts, William
TITLE OF INVENTION: HUMAN OSTECARTRITIS AND HUMAN PROTEASES

TITLE OF INVENTION: HUMAN OSTECARTRITIS AND HUMAN PROTEASES

FILE REFERENCE: 031896-043500 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,157

CURRENT FILING DATE: 2004-10-04

NUMBER OF SEQ ID NOS: 319805

SOFTWARE: Patentin version 3.2

SEQ ID NO 4751

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 22
 23 AsnGlnAlaAspHisPheLeuGlySerLeuAlaPheAlaLysLeu***ValArgThrLeu 42
 23 AsnGlnAlaAspHisPheLeuGlySerLeuAlaPheAlaLysLeu***ValArgThrLeu 42
 19 decedenterresadecesacesarraceración de la consecuenta de la consecuencia della d
 139 GCTGTCCCTTGGATTGAGTACCAGCATCACAAGCCTCCTTTCACCAACCTCCAT 195
 245 GCTGTCCCTCCTTGGATTGAGTACCAGCATCACAAGCCTCCTTTCACCAACCTCCAT 301
 3 AlaGlySerTrpAspLeuAlaGlyTyrLeuLeuTyr***Pro***MetGlyArgPheGly
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 Length:
Matches:
Conservative:
Mismatches:
Indels:
 Sequence 1, Application US/09774954
; Publication No. US20040241645A1
; GENERAL INFORMATION:
; TITLE OF INVENTION:
; CORRESPONDENCE ADDRESS:
; CORRESPONDENCE ADDRESS:
; STREET: 1 DNA WAY
; CITY: SOUTH SAN Francisco
; STATE: California
; COUNTRY: USA
 US-09-774-954-3 (1-61) x US-10-956-157-9986 (1-1400)
 US-09-774-954-3 (1-61) x US-10-956-157-4751 (1-1506)
Gabs:
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91.53$
91.53$
 TYPE: DNA
CORGANISM: Homo sapiens
US-10-956-157-4751
 ZIP: 94080
 Best Local Similarity:
Query Match:
 Percent Similarity:
 US-10-956-157-4751
 Alignment Scores:
Pred. No.:
 RESULT 5
US-09-774-954-1
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185 AACCAGGCCGATCACTTCTTGGGCTCTCTGGCATTTGCAAAGCTGCTAAACCGTACCTTG 244
 43 AlavalproprofrpileGluTyrGlnHisHisLysProProPheThrAsnLeuHis 61
 US-09-774-954-5

Sequence 5, Application US/09774954

Publication No. US20040241645A1

GENERAL INPORMATION:
TITLE OF INVENTION: O-PACOSyltransferase
NUMBER OF SEQUENCES: 17
CORMESSE Genentech, Inc.
STREET: 1 DNA May
CITY: South San Francisco
STRATE: California
COUMTRY: Gouth San Francisco
STATE: California
COMPUTER: Ealifornia
COMPUTER: SAD INCA
ILP: 94080

COMPUTER: ISM PC compactible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genetech)
CURRENT APPLICATION DATA:
PRIOR APPLICATION NAMER: US/09/774,954
FILING DATE: 26-NOV-1997

PRIOR APPLICATION NAMER: US/08/978,741
FILING DATE: 26-NOV-1997

APPLICATION NAMER: US/08/978,741
FILING DATE: 31-JAA-1997

APPLICATION NAMER: 39,044

REFERENCE/DOCKET NUMBER: 19,044

TELECOMMUTCATION NUMBER: 39,044

REFERENCE/DOCKET NUMBER: 19,044

TELECOMMUTCATION NUMBER: 39,044

REFERENCE/DOCKET NUMBER: 19,041P1

TELECOMMUTCATION NUMBER: 39,044

REFERENCE/DOCKET NUMBER: 19,041P1

TELECOMMUTCATION NUMBER: 39,044

REFERENCE/DOCKET NUMBER: 19,044

TELECOMMUTCATION NUMBER: 39,044

REFERENCE/DOCKET NUMBER: 11,1494

TELECOMMUTCATION NOMER: 30,042-1489

TELECOMMUTCATION NOMER: 30,043-1997

ATTORNEY/AGENT INFORMATION:
TELECOMMUTCATION NOMER: 39,044

REFERENCE/DOCKET NUMBER: 11,1494

TELECOMMUTCATION NOMER: 39,044

REFERENCE/DOCKET NUMBER: 11,1494

TELECOMMUTCATION NOMER: 30,045-1489

TELECOMMUTCATION NOMER: 30,045-1489

TELECOMMUTCATION NOMER: 30,045-1489

TELECOMMUTCATION NOMER: 30,045-1489

TELECOMMUTCATION NOMER: 30,045-1489

TELECOMMUTCATION NOMER: 30,045-1489

TELECOMMUTCATION NOMER: 30,045-1489

TELECOMMUTCATION NOMER: 30,045-1489

TELECOMMUTCATION NOMER: 30,045-1489
 11284
54
0
5
0
0
 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
 US-09-774-954-3 (1-61) x US-09-774-954-5 (1-11284)
 ;
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-774-954-5
 5.29e-32
295.00
91.53%
90.49%
 Percent Similarity:
Best Local Similarity:
Query Match:
DB:
 Alignment Scores:
Pred. No.:
 RESULT 8
US-09-774-954-5
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 RESULT 7

US-10-956-157-4752

US-10-956-157-4752

Sequence 4752, Application US/10956157

Seduence 4752, Application No. US20050118625A1

SEQUENCE INCORMATION:
APPLICANT: Wowth
TITLE OF INVENTION: UUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
FILE REFERENCE: 031896-643000 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,157

CURRENT FILING DATE: 2004-10-04

SUMMER: PATENTIN OST: 319805

SOUTWARE: PATENTIN VETSION 3.2

SEQ ID NO 4752

LENGTH: 5218
 23 AsnGlnAlaAspHisPheLeuGlySerLeuAlaPheAlaLysLeu***ValArgThrLeu 42
 5218
54
0
5
0
0
 5218
54
0
5
0
0
 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
 US-09-774-954-3 (1-61) x US-10-956-157-4752 (1-5218)
 US-09-774-954-3 (1-61) x US-10-301-822-168 (1-5218)
 PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR FILING DATE: 2002-03-05
PRIOR FILING DATE: 2002-05-20
NUMBER OF SEQ ID NOS: 228
SOFTWARE: FABLESEQ for Windows Version 4.0
LENGTH: 5218
 2.18e-32
295.00
91.53%
91.53%
 2.18e-32
295.00
91.53%
91.53%
 ; NAME/KEY: CDS
; LOCATION: (50)...(1216)
US-10-301-822-168
 TYPE: DNA
ORGANISM: Homo Sapiens
 Percent Similarity:
Best Local Similarity:
Query Match:
 Percent Similarity:
Best Local Similarity:
Query Match:
 Alignment Scores:
Pred. No.:
 Alignment Scores:
 Pred. No.:
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23 AsnGlnAlaAspHisPheLeuGlySerLeuAlaPheAlaLySLeu***ValArgThrLeu 42
 Sequence 18161, Application US/11097143
; Publication No. US20050208558A1
; Publication No. US20050208558A1
; Publication No. US20050208558A1
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE; TITLE OF INVENTION: DROSOPHILA GENES.
 2 AACCAGGCCGATCACTTCTTGGCCTCTCTGGCATTTGCAAAGCTGCTAAACCGTACCTTG
 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
 Length:
Matches:
Conservative:
Mismatches:
Indels:
 PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/978,741
FILING DATE: 26-NOV-1997
APPLICATION NUMBER: 08/792,498
FILING DATE: 31-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: 91041P1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
 US-09-774-954-3 (1-61) x US-09-774-954-7 (1-5009)
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/774,954
PILING DATE: 30-Jan-2001
CLASSIFICATION: <Unknown>
 Gaps:
 SEQUENCE DESCRIPTION: SEQ ID NO: 7:
 LENGTH: 5009 base pairs
 TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 7:
 STRANDEDNESS: Single
TOPOLOGY: Linear
 5.28e-19
204.00
94.87%
94.87%
 TYPE: Nucleic Acid
 Percent Similarity:
Best Local Similarity:
 RESULT 10
US-11-097-143-18161
 Alignment Scores:
Pred. No.:
RESULT 9
US-09-774-954-7
 US-09-774-954-7
 Query Match:
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APPLICANT: VELLEL, J. C. CIBIG

APPLICANT: et al.
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: DREASE, FOR DETECTING EXPRESSION OF 10,000 OR MORE
TITLE OF INVENTION: DRESCPHILA GENES.
TITLE OF INVENTION: DRESCPHILA GENES.
FILE REFRENCE: CLOOD.28
CURRENT APPLICATION NUMBER: US/11/097,143
CURRENT APPLICATION NUMBER: 60/157,832
PRIOR PILING DATE: 1999-10-05
PRIOR PILING DATE: 1999-10-19
PRIOR PILING DATE: 1999-10-19
PRIOR FILING DATE: 1999-10-28
PRIOR FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: 60/164,769
PRIOR APPLICATION NUMBER: 60/164,769
PRIOR APPLICATION NUMBER: 60/164,769
PRIOR APPLICATION NUMBER: 60/164,769
PRIOR APPLICATION NUMBER: 60/164,769
PRIOR APPLICATION NUMBER: 60/175,693
PRIOR APPLICATION NUMBER: 60/175,693
 27 HisPheleuGlySerLeuAlaPheAlaLysLeu**ValArgThrLeuAlaValProPto 46
 7 AspLeuAlaGlyTyrLeuLeuTyr***Pro***MetGlyArgPheGlyAsnGlnAlaAsp
 Conservative:
Mismatches:
Indels:
 US-09-774-954-3 (1-61) x US-11-097-143-18161 (1-1209)
 Length:
Matches:
FILE KEFERENCE: CLOOU ZAS
CURRENT PELLING DATE: 2006-04-04
PRIOR APPLICATION NUMBER: 00/157,832
PRIOR FILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-10-05
PRIOR FLING DATE: 1999-10-19
PRIOR FLING DATE: 1999-10-19
PRIOR PELLING DATE: 1999-10-28
PRIOR PELLING DATE: 1999-10-28
PRIOR PELLING DATE: 1999-10-28
PRIOR FILING DATE: 1999-11-12
PRIOR PELLING DATE: 1999-11-12
PRIOR FILING DATE: 1999-10-28
PRIOR FILING DATE: 2099-11-28
PRIOR FILING DATE: 2000-01-12
PRIOR FILING DATE: 2000-01-12
PRIOR PILING DATE: 2000-01-13
PRIOR PILING DATE: 2000-01-15
PRIOR PILING DATE: 2000-01-15
PRIOR PILING DATE: 2000-01-15
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PRIOR PILING DATE: 2000-01-15
PRIOR PILING DATE: 2000-01-15
PRIOR PILING DATE: 2000-01-15
 Sequence 18160, Application US/11097143; Publication No. US20050208558A1; GENERAL INFORMATION:
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 47 TrpileGluTyrGln 51
 177.00
80.00%
73.33%
54.29%
 Percent Similarity:
Best Local Similarity:
Query Match:
 RESULT 11
US-11-097-143-18160/c
 US-11-097-143-18161
 Alignment Scores:
 TYPE: DNA
 ORGANISM:
 ..
No.:
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0.281
76.00
83.33
77.78
23.31%
 44.48%
26
 ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-602444
 Percent Similarity:
Best Local Similarity:
Query Match:
DB:
 US-10-820-474A-236
 Alignment Scores:
 APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
 Query Match:
DB:
 RESULT 12
US-11-097-143-18082/c

Sequence 18082, Application US/11097143

Publication No. US2005020858A1

SEQUENCEL INFORMATION:

APPLICANT: Venter, J. Craig

APPLICANT: Venter, J. Craig

APPLICANT: Venter, J. Craig

TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID

TITLE OF INVENTION: DECOSOPHILA GENES.

TITLE OF INVENTION: DECOSOPHILA GENES.

TITLE OF INVENTION: DECOSOPHILA GENES.

FILE REFERENCE: CLOO0728

CURRENT FILING DATE: 100729

PRIOR FILING DATE: 1999-10-05

PRIOR FILING DATE: 1999-10-19

PRIOR PLILING DATE: 1999-10-28

PRIOR PLILING DATE: 1999-10-28

PRIOR FILING DATE: 1999-11-12

PRIOR FILING DATE: 1999-11-12

PRIOR FILING DATE: 1999-11-12

PRIOR FILING DATE: 1999-10-28

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PRIOR FILING DATE: 1999-10-28

PRIOR FILING DATE: 1999-10-28

PRIOR FILING DATE: 2000-02-24

PRIOR FILING DATE: 2000-03-23

NUMBER OF SEQ ID NOS: 43008

SOFTWARE: PRESENCE for Windows Version 4.0

SEQ ID NO 18082

DATE OF THE DATE OF THE DATE OF THE O
 39 ValArgThrLeuAlaValProProTrpIleGluTyrGln 51
2032 AATCGCACCCTGATCCTCGCCGCCGTGGGTGGAGTATCGT 1994
 Length:
Matches:
Conservative:
Mismatches:
 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
 US-09-774-954-3 (1-61) x US-11-097-143-18160 (1-3264)
FRIOR FILING DATE: 2000-01-12
FRIOR PILING DATE: 2000-02-44
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FRIOR FILING DATE: 2000-03-23
FRIOR FILING DATE: 2000-03-23
FRIOR FILING PATE: 2000-03-23
FRIOR FILING DATE: 2000-03-23
FRIOR
 1.58e-10
145.00
87.88%
78.79%
 1.88e-10
145.00
87.88%
78.79%
 ; TYPE: DNA
; ORGANISM: DROSOPHILA
US-11-097-143-18160
 TYPE: DNA
CRGANISM: DROSOPHILA
US-11-097-143-18082
 Percent Similarity:
Best Local Similarity:
Query Match:
 Percent Similarity:
Rest Local Similarity:
 Alignment Scores:
Pred. No.:
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| Query Watch: 24.48# Indels: 0 | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operation | Operatio
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117 gegggerecregadecegecegerracrecreratececerecargagara 170
 3 AlaGlySerTrpAspLeuAlaGlyTyrLeuLeuTyr***Pro***MetGlyArg 20
APPLICANT: BANDMAN, OLGA
TITLE OF INVENTION: SIGNL PEPTIDE-CONTAINING MOLECULES
FILE REFERENCE: 039386-1568
CURRENT PELING NUMBER: US/10/820,474A
CURRENT FILING DATE: 2004-04-07
PRIOR FILING DATE: 2004-03-20
PRIOR FILING DATE: 1999-06-25
PRIOR FILING DATE: 1999-06-25
PRIOR FILING DATE: 1998-06-26
PRIOR PELICATION NUMBER: 60/090,762
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PRIOR APPLICATION NUMBER: 60/090, 762
PRIOR PELING DATE: 1998-07-31
PRIOR PELING DATE: 1998-07-31
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PRIOR PELING DATE: 1998-07-31
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PRIOR PELING DATE: 1998-10-01
NUMBER OF SEQ ID NOS: 269
SOFTWARE: PATENTIN VETSION 3.3
SOFTWARE: PATENTIN VETSION 3.3
 1803
23
 760
14
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0
 Length:
Matches:
Conservative:
Mismatches:
Indels:
 US-09-774-954-3 (1-61) x US-10-820-474A-236 (1-760)
 Length:
Matches:
 JOS-10-126 701-30

JOS-10-126 701-30

JOS-10-126 701-30

Publication No. US20030119018A1

GENERAL INFORMATION:
JAPPLICANT: OWURA, SATOSHI

APPLICANT: ISHIKAWA, JUN

APPLICANT: SHIRAWA, JUN

APPLICANT: SHIRAWA, JUN

APPLICANT: SHIRAWA, HROSHI

APPLICANT: SHIRAWA, HROSHI

APPLICANT: SHIRAWA, HROSHI

APPLICANT: SAIBA, TADAYOSHI

APPLICANT: SAIBA, TADAYOSHI

APPLICANT: SAIBA, TADAYOSHI

APPLICANT: BATTORI, MASAHIRA

TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES

FILE REPERENCE: 249-262

CURRENT APPLICATION NUMBER: US 2001-204089

PRIOR FILING DATE: 2001-05-30

PRIOR FILING DATE: 2001-05-30

PRIOR FILING DATE: 2001-05-30

PRIOR FILING DATE: 2001-05-30

SHOR FILING DATE: 2001-05-30

SHOR FILING DATE: 2001-05-30

NUMBER OF SEQ ID NOS: 15109
 ; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte Clone No: 1647884
US-10-820-474A-236
 TYPE: DNA ORGANISM: Streptomyces avermitilis
 0.433
76.00
83.33$
77.78$
23.31$
 3.83
 TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
 , LOCATION: (1)..(1803)
US-10-156-761-5001
 Percent Similarity:
Best Local Similarity:
Query Match:
 RESULT 15
US-10-156-761-5001
 FEATURE:
NAME/KEY: CDS
 Alignment Scores:
Pred. No.:
Score:
 Alignment Scores:
Pred. No.:
 Score:
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---- AACACCTCTACGTACCGCCGAAGGCCTTCTTCGAC 342
 5 SerTrpAspLeuAlaGlyTyrLeuLeuTyr***Pro***MetGlyArgPheGlyAsnGln 24
 ------GlySer 31
 ------ 46
 343 GACCCGCAGTGGAAGGACATCACCGACTGCAGGAGGAACTGAAGCCGTAC 393
 47 ------Trp-----IleGluTyrGlnHisHisLysProProPhe 57
 32 LeualaPheAlaLysLeu***ValArgThrLeuAlaValProPro-
 8
17
59
 25 AlaAspHisPheLeu-------
 Conservative:
 US-09-774-954-3 (1-61) x US-10-156-761-5001 (1-1803)
 Mismatches:
Indels:
Gaps:
 Search completed: October 26, 2005, 16:00:04 Job time : 287.326 secs
 40.26%
29.87%
22.24%
16
 295 CTCAACTACGCG----
Percent Similarity:
Best Local Similarity:
Query Match:
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Sequence

Sequence 11934, A Sequence 2414, Ap Sequence 1007, Ap Sequence 1, Appli Sequence 1, Appli Sequence 20391, Sequence 17504, A Sequence 17504, A Sequence 2, Appli Sequence 2, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli

Sequence 10,

Sequence 9,

Sequence

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US-09-107-433-1007
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 601
276237
175265
154600
 2352
2352
18627
 3791
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 61.5
61.5
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61.5
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 October 26, 2005, 08:18:39 ; Search time 53.4846 Seconds (without alignments) 1866.199 Million cell updates/sec
 1 RLAGSWDLAGYLLYXPXMGR.....LAVPPWIEYQHHKPPFTNLH
 2405568
 GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
 nucleic search, using frame_plus_p2n model
 Total number of hits satisfying chosen parameters:
 1202784 segs, 818138359 residues
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
 Minimum DB seq length: 0
Maximum DB seq length: 2000000000
 US-09-774-954-3
326
 BLOSUM62
 Title:
Perfect score:
 Scoring table:
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Sequence:

Sequence 5482, Ap Sequence 3, Appli

Sequence 3, Sequence 5, Sequence 5,

Sequence 5

Sequence Sequence

Sequence 4, Sequence 2,

Sequence Sequence Sequence

Sequence

Sequence 3, Appli Sequence 17224, A

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CCMPUTER READBLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 1DM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,741
FILING DATE: 26-No. 6100076-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/792498
 Sequence 16, Application US/08978741
; Sequence 16, Application US/08978741
; Patent No. 610076
; GENERAL INFORMATION:
 TITLE OF INVENTION: O-Pucosyltransferase
; TITLE OF INVENTION: O-Pucosyltransferase
; CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 1 DNA Way
 CITY: South San Francisco
; STREE: California
; COUNTRY: USA
 NAME: SVODOda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P1041P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
TELEFAR: 650/922-9881
INFORMATION FOR SEQ ID NO: 16: SEQUENCE CHARACTERISTICS:
 FILING DATE: 31
ATTORNEY/AGENT INFORMATION:
 ZIP: 94080
US-08-978-741-16
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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12. /Ggn2\_6/prodaca1/ina/5B\_COMB.seq:\*
31. /Ggn2\_6/prodaca1/ina/6A\_COMB.seq:\*
41. /Ggn2\_6/prodaca1/ina/6B\_COMB.seq:\*
42. /Ggn2\_6/prodaca1/ina/6B\_COMB.seq:\*
43. /Ggn2\_6/prodaca1/ina/PCTUS\_COMB.seq:\*
44. /Ggn2\_6/prodaca1/ina/PCTUS\_COMB.seq:\*
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Database

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1100 1100 1300 1514 11284 10284 5009 19227

Description

DB

Query Match Length

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 23 AsnGlnAlaAspHisPheLeuGlySerLeuAlaPheAlaLysLeu***ValArgThrLeu 42
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 3 AlaglySerTrpAspLeuAlaglyTyrLeuLeuTyr***Pro***MetGlyArgPheGly 22
 43 AlaValProProTrpIleGluTyrGlnHisHisLysProProPheThrAsnLeuHis 61
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54
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5
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54
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Matches:
Conservative:
Mismatches:
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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 US-09-774-954-3 (1-61) x US-08-978-741-16 (1-1100)
 US-001-333-729A-16
Sequence 16, Application US/09333729A
Farent No. 6270847
GENERAL INFORMATION:
APPLICANT: Wang Yang
TITLE OF INVENTION:
FILE REFREENCE PIO41PID1-Substitute
CURRENT APPLICATION NUMBER: US/09/333, 729A
CURRENT PILING DATE: 1999-06-15
PRIOR FILING DATE: 1999-06-15
NUMBER OF SEQ ID NOS: 21
LENGTH: 1100
 Gaps:
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US-08-978-741-4
, Sequence 4, Application US/08978741
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295.00
91.53%
90.49%
 5.56e-36
295.00
91.53$
91.53$
LENGTH: 1100 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
 TYPE: DNA
CORGANISM: Homo Sapien
US-09-333-729A-16
 Percent Similarity: 5 Best Local Similarity: 9 Query Match: 9 DB:
 Percent Similarity:
Best Local Similarity:
Query Match:
 Alignment Scores:
Pred. No.:
 Alignment Scores:
Pred. No.:
 US-08-978-741-16
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Alignment Scores:
Pred. No.:
 Alignment Scores:
 LENGTH: 1514
 RESULT 6
US-09-333-729A-2
 US-09-333-729A-2
 US-08-978-741-5
 Query Match:
DB:
 Query Match
 Pred. No.:
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 23 AsnGlnAlaAspHisPheLeuGlySerLeuAlaPheAlaLysLeu***ValArgThrLeu 42
 3 AlaGlySerTrpAspLeuAlaGlyJyrLeuLeuTyr***Pro***MetGlyArgPheGly
 Sequence 1, Application US/08978741
; Sequence 1, Application US/08978741
; Patent No. 6100076
; GENERAL INFORMATION:
 TITLE OF INVENTION: O-Fucosyltransferase
 NUMBER OF SEQUENCES: 17
 CORRESPONDENCE ADDRESS: 17
 CORRESPONDENCE ADDRESS: 17
 COUNTRY: South San Francisco
 STREET: I DAN Way
 CITY: South San Francisco
 STREET: USA
 IP DAN WAY
 CITY: South San Francisco
 STREE: California
 COUNTRY: BADABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: EMP C compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WinPatin (Genentech)
 COMPUTER: IS NOTEM: BAPPLICATION NOTE: 31
 APPLICATION NUMBER: US/08/978,741
 FILING DATE: 26-NO. 6100076-1997
 CLASSIFICATION NUMBER: 08/792498
 FILING DATE: 35
 PRIOR APPLICATION NUMBER: 08/792498
 FILING DATE: 37
 ATTORNEY AGENT INFORMATION:
 NAME: Svoboda, Craig G.
 REFERENCE/DOCKET NUMBER: P1041P1
 TELEFONMULCATION INFORMATION:
 TELEFONMULCATION INFORMATION:
 TELEFONMULCATION PROPARATION:
 TELEFONMULCATION PROPA
 Conservative:
Mismatches:
Indels:
 US-09-774-954-3 (1-61) x US-09-333-729A-6 (1-1300)
 Length:
Matches:
 Gaps:
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 TYPE: DNA
ORGANISM: Artificial Sequence
 TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
 1997-11-26
 6.98e-36
295.00
91.53%
91.53%
 LENGTH: 1514 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
PRIOR FILING DATE: 19
NUMBER OF SEQ ID NOS:
SEQ ID NO 6
 TOPOLOGY: Linear
 Percent Similarity:
Best Local Similarity:
 Alignment Scores:
 LENGTH: 1300
 US-08-978-741-1
 FEATURE:
 Query Match:
DB:
 Pred. No.:
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 23 AsnGlnAlaAspHisPheLeuGlySerLeuAlaPheAlaLysLeu***ValArgThrLeu 42
 99
 23 AsnGlnAlaAspHisPheLeuGlySerLeuAlaPheAlaLysLeu***ValArgThrLeu 42
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Mismatches:
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 Sequence 2, Application US/0933729A
; Sequence 2, Application US/0933729A
; GENERAL INFORMATION:
APPLICANT: Wang, Yang
APPLICANT: Spellman, Michael W.
ITLE OF INVENTION: O-Fucosyltransferase
FILE REFERENCE: P1041P1D1-Substitute
CURRENT APPLICATION NUMBER: US/09/333,729A
CURRENT FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: US 08/798,741
; PRIOR FILING DATE: 1997-11-26
 APPLICANT: Yang Wang, Michael W. Spellman
TITLE OF INVENTION: O-Fucosyltransferase
NUMBER OF SEQUENCES: 17
 Length:
Matches:
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 ; Sequence 5, Application US/08978741; Patent No. 6100076; GENERAL INFORMATION:
8.58e-36
295.00
91.53%
91.53%
 8.58e-36
295.00
91.53%
91.53%
 NUMBER OF SEQ ID NOS: 21
SEQ ID NO 2
 TYPE: DNA
ORGANISM: Homo Sapien
 Percent Similarity:
Best Local Similarity:
 Percent Similarity:
Best Local Similarity:
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US-09-774-954-3 (1-61) x US-09-333-729A-8 (1-5009)
 Query Match:
DB:
 à
 Length:
Matches:
Conservative:
Mismatches:
Indels:
 US-08-9/80/14-pplication US/08978741
| Sequence 7, Application US/08978741
| Patent No. 6100076
| GENERAL INFORMATION: OF LOCOSTICE OF INVENTION: OF PLOCOSTICE OF INVENTION: OF PLOCOSTICE OF INVENTION: OF CORRESPONDENCE ADDRESS: 17
| CORRESPONDENCE ADDRESS: ADDRESSE: Genemech, Inc. | STREET: 1 DNA Way CITY: South San Francisco | STRAET: California COUNTRY: USA | COUNTRY: USA | COUNTRY: USA | COUNTRY: USA | COUNTRY: USA | COUNTRY: WARDABLE FORM: COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
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 1.32e-34
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91.53%
90.49%
 Percent Similarity:
Best Local Similarity: 9
Query Match:
DB:
 , TOPOLOGY: Linear
US-08-978-741-5
 Alignment Scores:
Pred. No.:
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Length:
Matches:
Conservative:
Mismatches:
 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
 US-09-774-954-3 (1-61) x US-08-978-741-7 (1-5009)
 WESOLI 9
US-05-33-729A-8
Sequence 8, Application US/0933729A
Sequence 8, Application US/0933729A
Parent No. 6270987
APPLICANT: Wang Yang
TITIE OF INVENTION: O-Fucosyltransferase
TITIE OF INVENTION: O-Fucosyltransferase
TITIE REPERBNCE: P1041P1D1-Substitute
CURRENT FILING DATE: 1999-06-15
FRIOR PALLICATION NUMBER: US/09/333,729A
CURRENT FILING DATE: 1999-06-15
FRIOR PALLICATION NUMBER: US 08/798,741
FRIOR FILING DATE: 1997-11-26
NUMBER OF SEQ ID NOS: 21
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION NATA:
APPLICATION NAMBER: US/08/978,741
FILING DATE: 26-No. 6100076-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/792498
FILING DATE: 31
ATTORNEY/AGENT INFORMATION:
NAME: SYODODA, CTAIG G.
NAME: SYODODA, CTAIG G.
REDISTARTION NUMBER: P1041P1
FELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELERAN: 650/252-9881
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: SOO9 base pairs
TYPE: NUCLEC Acid
TYPE: NUCLEC Acid
TYPE: NUCLEC Acid
TYPE: NUCLEC Acid
TYPE: NUCLEC Acid
TYPE: NUCLEC Acid
TYPE: TOPOLOGY: Linear
US-08-978-741-7
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94.87$
94.87$
62.58$
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204.00
94.87%
94.87%
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US-09-333-729A-8
 Percent Similarity:
Best Local Similarity:
Query Match:
DB:
 Percent Similarity:
Best Local Similarity:
 Alignment Scores:
Pred. No.:
 Alignment Scores:
Pred. No.:
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SEQ ID NO 16285
 LENGTH: 19228
 Alignment Scores:
Alignment Scores:
Pred. No.:
 TYPE: DNA
 Query Match:
DB:
 Pred. No.:
 g
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 Sequence 12127, Application US/09949016

Sequence 12127, Application US/09949016

Sequence 12127, Application US/09949016

Sequence 12127, Application US/09949016

Sequence 12127, Application US/09949016

GENERAL INFORMATION:

APPLICAMT: VENTION:

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: PSELES OF WINDOWS Version 4.0

LENGTH: 19227
 27 HisPheleuGlySerLeuAlaPheAlaLysLeu***ValArgThrLeuAlaValProPro 46
 2 AACCAGGCCGATCACTTCTTGGGCTCTCTGGCATTTGCAAAGCTGCTAAACCGTACCTTG 61
 AsnGlnAlaAspHisPheLeuGlySerLeuAlaPheAlaLysLeu***ValArgThrLeu 42
 Sequence 14333, Application US/09270767

Batent No. 6703491

GENERAL INFORMATION:
GENERAL INFORMATION:

APPLICANT: Homburger et al.

TITLE OF INVERNICS: File Reference: 7326-094

CURRENT APPLICANT: 1999-03-17

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT PILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 14353

LENGTH: 1320
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 7 AspLeuAlaGlyTyrLeuLeuTyr***Pro***MetGlyArgPheGlyAsnGlnAlaAsp
 43 AlaValProProTrpIleGluTyrGlnHisHisLysProProPheThrAsnLeuHis 61
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Matches:
Conservative:
Mismatches:
Indels:
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; ORGANISM: Drosophila melanogaster
US-09-270-767-14353
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195 TGGGTGGAGTATCGT 209
 1.43e-17
177.00
80.00%
73.33%
54.29%
 47 TrpIleGluTyrGln 51
 Percent Similarity:
Best Local Similarity:
Query Match:
 ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12127
 RESULT 10
US-09-270-767-14353
 Alignment Scores:
Pred. No.:
 ઠે
 В
```

```
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITILE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REPERENCE: CL001307
GURRENT APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
 Sequence 131, Application US/08311731A

Sequence 131, Application US/08311731A

Patent No. 6583266

GENERAL INFORMATION:
APPLICANT: SMITH, DOUGLAS

APPLICANT: MAO, JEN-1

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES

TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

NUMBER OF SEQUENCES: 411

CORRESPONDENCE ADDRESS:
 1712 GCGGGCTCCTGGGACCCGGCCGGTTACCTGCTCTACTGCCCCTGCATGGGTAAG 1659
 1712 écedecricordedeccedecederraciderretracrecécerecardedrang 1659
 US-09-774-954-3 (1-61) x US-09-949-016-16285 (1-19228)
 Length:
Matches:
Conservative:
Mismatches:
Indels:
 US-09-774-954-3 (1-61) x US-09-949-016-12127 (1-19227)
Length:
Matches:
Conservative:
Mismatches:
 ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C. STREET: 600 ATLANTIC AVENUE
 Indels:
 Gaps:
 US-09-949-016-16285/c
; Sequence 16285, Application US/09949016
; Patent No. 6812339
 ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
2.55
76.00
83.33
77.78
 CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
 Percent Similarity:
Best Local Similarity:
Query Match:
 Percent Similarity:
Best Local Similarity:
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US-08-311-731A-131/c
 ; ORGANISM: Human
US-09-949-016-16285
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; LENGTH: 266293
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-11934
 Alignment Scores:
Pred. No.:
 Alignment Scores:
 TYPE: DNA
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 RESULT 14
US-09-949-016-11934
US-09-949-016-11934
Sequence 11934, Application US/09949016
Fatent No. 6812339
GENERAL INPORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01307
CURRENT PAPLICATION NUMBER: 60/241,755
FRIOR FILING DATE: 2000-04-14
FRIOR APPLICATION NUMBER: 60/241,756
FRIOR APPLICATION NUMBER: 60/231,768
FRIOR PILING DATE: 2000-010-03
FRIOR PILING DATE: 2000-010-03
FRIOR FILING DATE: 2000-010-03
FRIOR FILING DATE: 2000-010-03
FRIOR FILING DATE: 2000-09-08
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FRIOR FILING DATE: 2001-10-03
FRIOR FILING DAT
 30298 TCCTGGGATCTGCGTAAATTC---CTCTGGGGCGCCGAAGCTGGGCTGCGTACGAAAGTCGAAAGT
 30181 TTGAACTACGCG------ 30149
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 5 SerTrpAspLeuAlaGlyTyrLeuLeuTyr***Pro***MetGlyArgPheGlyAsnGln 24
 25 AlaAspHisPheLeu-----GlySer 31
 32 LeuAlaPheAlaLysLeu***ValArgThrLeuAlaValProProTrpIleGluTyrGln 51
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PILING DATE:
FILING DATE:
CLASSIFICATION: 530
 Length:
Matches:
Conservative:
Mismatches:
Indels:
 US-09-774-954-3 (1-61) x US-08-311-731A-131 (1-42325)
 ATTORNEY AGENT INFORMATION:
NAME: GATES, EDWARD R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: 0044/7125
RELECHONICATION INFORMATION:
TELECHONICATION INFORMATION:
TELEPHONE: 617/720-3500
INFORMATION FOR SEQ ID NO: 131:
SEQUENCE CHARACTERISTICS:
LENGTH: 42325 base pairs
TYPE: nucleic acid
STRANDENNESS: double
TYPE: nucleic acid
STRANDENNESS: double
TYPE: nucleic acid
STRANDENNESS: double
TYPE: NO GATES IN ON GENOMIC)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ANTI-SENSE: NO
RAITAL SOURCE:
ORGANISM: MYCOBACTERIUM LEPRAE
 30148 -----GAGCCGTTCTTTGCCAAC 30131
 52 HisHisLysProProPheThrAsn 59
 109
68.50
42.65%
33.82%
21.01%
 Percent Similarity: 4
Best Local Similarity: 3
Query Match:
 Alignment Scores:
Pred. No.:
 셤
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VS-09-583-110-2414

is Sequence 2414, Application US/09583110

is Sequence 2414, Application US/09583110

is Sequence 2414, Application US/09583110

is Sequence 2414, Application US/09583110

is APPLICANT: Lynn Doucette-Stamm et al.

is TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus

is TITLE OF INVENTION: PARHOLO-07A

is TITLE OF INVENTION: PARHOLO-07A

is TITLE OF INVENTION: PARHOLO-07A

is CURRENT FILING DATE: 2000-05-26

is PRIOR PAPLICATION NUMBER: US 09/107,433

is PRIOR FILING DATE: 1998-06-30

is PRIOR FILING DATE: 1998-06-30

is PRIOR FILING DATE: 1998-06-30

is PRIOR FILING DATE: 1998-06-30

is PRIOR FILING DATE: 1997-07-02

is PRIOR FILING DATE: 1997-07-02

is DRIOR FILING DATE: 1997-07-02
 236286 CTCCACCTTCATGACTTAGTCATCCCCCAGTGGTCCCACCTTCTAATACCATCACCTCAG 236345
 418 irdarcdGGGrcGcrcrrrararrccaacagccrrrcrrrrrcaaararcggaactrac 477
 ||||:::|||||||::
478 TITATIGGITCTATCTIG-----ATITIAGIGGGITCICICCTAGICAGCCCIIGG 528
 28 PheLeuGlySerLeuAlaPheAlaLysLeu***ValArgThrLeuAlaValProProTrp 47
 8 LeuAlaGlyTyrLeuLeuTyr***Pro***MetGlyArgPheGlyAsnGlnAlaAspHis 27
 21 PheglyAsnGlnAlaAspHisPheLeu------GlySerLeuAlaPheAlaLys--- 36
 37 Leu***ValArgThrLeuAlaValProProTrp-----------
266293
19
11
22
14
 US-09-774-954-3 (1-61) x US-09-949-016-11934 (1-266293)
 Length:
Matches:
Conservative:
Mismatches:
Indels:
 Length:
Matches:
Conservative:
Mismatches:
 US-09-774-954-3 (1-61) x US-09-583-110-2414 (1-2214)
 Gaps:
 236346 GAGTTAGAATTTCAACAT 236363
), ORGANISM: Streptococcus pneumoniae US-09-583-110-2414
 48 --- IleGluTyrGlnHis 52
 67.00
45.45%
28.79%
20.55%
 4.01
66.50
48.84%
37.21%
20.40%
 Percent Similarity:
Best Local Similarity:
Query Match:
DB:
 Percent Similarity:
Best Local Similarity:
Query Match:
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48 IleGluTyr 50 ||| 529 TCTGTTTAC 537

\$ g

Search completed: October 26, 2005, 15:25:31 Job time: 106.485 secs

(otazu) XNAJA 3DAY ZINT

Human pol First Eco Drosophil

OM protein

Run on:

Sequence:

Searched:

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Aca9853 Streptoco
Aca49857 Prokaryot
Aax16136 DNA encod
Aav52246 Streptoco
Continuation (8 of
Adb56839 Primary r
Add56829 Toxicity
Add56829 Toxicity
Add57980 Human can
Adi13371 Mouse LPD
Adi3371 Mouse LPD
Adi23371 Mouse LPD
Aca49002 Prokaryot
Ada69987 Rice gene
Ada69987 Rice gene
Ada69987 Rice gene
Ada69987 Rice gene
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Ada69987 Rice gene
Ada69987 Rice gene
Ada69987 Rice gene
Ada69987 Rice gene
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Ada69987 Rice gene
Ada69987 Rice gene
Ada69988 Human imm
Ab193098 Rat metas
Adn07889 Human imm
Ab19309 Prokaryot
 Abli3947 Drosophil
Abli3946 Drosophil
Abli3949 Drosophil
Az298210 Human sig
Aca37736 Prokaryot
AdA74382 Mycobacte
Adb53234 Primary r
Az296329 S. pneumo
Abx06561 S. pneumo
Abx06561 S. preumo
Abx06555608 Streptoco
Aas55608 Streptoco
 Ado58598 Porcine a
Acn44612 Mouse gen
Continuation (4 of
Abd33038 Mouse can
 O-fucosyltransferase; epidermal growth factor; EGF; glycosylation;
O-fucose; inhibitor; sensory neuron; retinal neuron; human; heart; ss.
 Human heart O-fucosyltransferase encoding DNA
 ALIGNMENTS
 ABS56454_07
ADB50839
ABT40319
 AAI61373 0
AAI61373 1
ADJ75816
 ACA49002
ADA69987
AAKB3286
ACH76865
AAK84657
ABL93098
 ADN07889
ABL11790
 10 ABX06561
13 ADR92372
3 AAA05535
4 AAS55608
4 AAS5863
2 AAX16136
2 AAX16136
2 AAX52246
 ADB56829
ADQ97980
 ABA03041 C
 AAZ98210
ACA37736
ADB74382
 ADB53234
AAZ96329
 ABD33038
 AAV65634
ABL13947
ABL13946
 ACA36930
 ABL13894
 AAV65632 standard; DNA; 1514 BP.
 97WO-US023401
 16-DEC-1998 (first entry)
 73507
110000
8455
 510
5983
577
 18627
110000
 110000
 2155
1018
1580
4184
 3793
760
760
594
42325
2720
1660
 22292
2304
2304
2304
2351
 97081
 Homo sapiens
 misc_feature
 17-DEC-1997;
 409833924-A1
 06-AUG-1998.
 62.5
62.5
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 64.5
 63.5
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 AAV65632;
 RESULT 1
 AAV65632
υ
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 Aav65632 Human hea
Acn40746 Tumour-as
Adf81754 Leukaemia
Aav65633 Plasmid c
Aax51510 Human pol
 October 26, 2005, 03:15:37; Search time 170.85 Seconds (without alignments) 2113.573 Million cell updates/sec
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 Description
 1 RLAGSWDLAGYLLYXPXMGR.....LAVPPWIEYQHHKPPFTNLH
 8780412
 GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
 nucleic search, using frame_plus_p2n model
 Total number of hits satisfying chosen parameters:
 4390206 segs, 2959870667 residues
 SUMMARIES
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 AAV65632
ACN40746
ADF81754
AAV65633
AAK51510
 0.5
7.0
7.0
 Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
 geneseqn2003cs:*
 geneseqn2003ds:*
 geneseqn2004as:*
geneseqn2004bs:*
 geneseqn2001as:*
 geneseqn2001bs:*
 geneseqn2002as:*geneseqn2002bs:*
 geneseqn2003as:*
 geneseqn2003bs:*
 Geneseq 16Dec04:*
Geneseqn1980s:*
 geneseqn1990s:*
 geneseqn2000s:*
 Minimum DB seq length: 0
Maximum DB seq length: 2000000000
 13
 Query
Match Length DB
 10
 US-09-774-954-3
326
 1514
5218
5266
11284
5230
 BLOSUM62
 10:
 . 295
295
295
295
232.5
 Score
 Title:
Perfect score:
 Scoring table:
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Database

Š. Result

N

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15-APR-2004
 ADF81754;
 Query Match:
DB:
 Wu TD,
 ADF81754
ID ADF8
XX
AC ADF8
XX
DT 26-F
 RESULT 3
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 This DNA encodes a human heart O-fucosyltransferase that can glycosylate an epideranal growth factor (EGF) domain of a polypeptide with an activated O-fucose residue. Inhibitors of O-fucosyltransferase, e.g. mutants with increased affinity for the EFG domains, are used in diagnosis and treatment of conditions associated with overexpression of O-fucosyltransferase, to promote survival of sensory (retinal) neurons. Probes based on EGF domain polypeptide are used to detect gene amplification and expression. The expression can also be determined at the protein level using antibodies specific for O-fucosyltransferase
 67 AACCAGGCCGATCACTTCTTGGGCTCTCTGGCATTTGCAAAGCTGCTAAACCGTACCTTG 126
 99
 23 AsnGlnAlaAspHisPheLeuGlySerLeuAlaPheAlaLysLeu***ValArgThrLeu 42
 Tumour-associated antigenic target; TAT; human; overexpression; tumour; diagnosis; cell proliferative disorder; breast cancer; colorectal cancer; lung cancer; ovarian cancer; liver cancer; central nervous system cancer; bladder cancer; pancreatic cancer; certrical cancer; melanoma; leuksemia; hybridisation probe; chromosome identification; chromosome mapping; chromosome identification; chromosome mapping;
 Tumour-associated antigenic target (TAT) cDNA DNA326813, SEQ ID NO:5725
 Human O-fucosyl:transferase able to glycosylate epidermal growth factor domains - useful for diagnosis and treatment of diseases involving overexpression of the enzyme.
 7 GCGGGCTCCTGGGACCCGGCCGGTTACTGCTTACTGCCCCCTGCATGGGGCTTTTGGG
 3 AlaGlySerTrpAspLeuAlaGlyTyrLeuLeuTyr***Pro***MetGlyArgPheGly
 Sequence 1514 BP; 320 A; 435 C; 411 G; 348 T; 0 U; 0 Other;
 Length:
Matches:
Conservative:
Mismatches:
Indels:
 Gaps:
 US-09-774-954-3 (1-61) x AAV65632 (1-1514)
 ACN40746 standard; cDNA; 5218 BP
 Claim 9; Fig 12A; 90pp; English.
 31-JAN-1997; 97US-00792498.
26-NOV-1997; 97US-00978741.
 5.87e-33
295.00
91.53%
91.53%
 (first entry)
 (GETH) GENENTECH INC.
 Wang Y, Spellman MW;
 WPI; 1998-437477/37.
P-PSDB; AAW80571.
 Similarity:
 WO2004030615-A2
 Percent Similarity:
 18-NOV-2004
 Homo sapiens
 Alignment Scores:
 ACN40746;
 Best Local Si
Query Match:
DB:
 RESULT 2
 ACN40746
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The invention relates to human tumour-associated antigenic target (TAT) polypeptides, and their related nucleic acids. The TAT polypeptides are overexpressed in cancer tissues compared to normal tissues, and may thus serve as effective targets for the diagnosis and treatment of cancer in mammals. The invention also relates to nucleic acid and polypeptide normals. The invention also relates to nucleic acid and polypeptide oplypeptides and though specific for a TAT polypeptide; and methods specific for a TAT polypeptide; appetide or organic acid, an antibody specific for a TAT polypeptide; proteins comprising a TAT norleagh which binds to a TAT polypeptide; nucleic acids, antibodies, antagonists, binding molecules and compositions are useful.

TAT polypeptide, antagonists, binding molecules and compositions are useful.

TAT polypeptides are treating a call proliferative disorder associated with for diagnosing or treating a call proliferative disorder associated with concreased TAT expression, particularly ancers such as breast cancer, colorectal cancer, lung cancer, ovarian cancer, bladder cancer, lung cancer, ovarian cancer, bladder cancer, pancreatic cancer, ovarian cancer, bladder cancer, bladder cancer, ovarian cancer, bladder cancer, bladder cancer, ovarian cancer, bladder cancer, bladder cancer, ovarian cancer, bladder cancer, bladder cancer, ovarian cancer, bladder cancer, bladder cancer, orangements and leukaemia. TAT nucleic acids may further be used as hybridisation probes, in chromosome and gene mapping, in chromosome identification and in gene furrance and gene mapping, in chromosome identification and in gene furrance.
 244
 3 AlaGlySerTrpAspLeuAlaGlyTyrLeuLeuTyr***Pro***MetGlyArgPheGly
 New tumor-associated antigenic target polypeptides and nucleic acids, useful in preparing a medicament for treating or detecting a proliferative disorder, e.g. breast, lung, colorectal, ovarian or
 Sequence 5218 BP; 1255 A; 1274 C; 1334 G; 1355 T; 0 U; 0 Other;
 5218
54
0
5
0
0
 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
 Claim 1; SEQ ID NO 5725; 7273pp; English.
 US-09-774-954-3 (1-61) x ACN40746 (1-5218)
 ADF81754 standard; DNA; 5266 BP
29-SEP-2003; 2003WO-US028547.
 02-OCT-2002; 2002US-0414971P.
 2.856-32
295.00
91.53%
91.53%
 (first entry)
 prostate cancer or tumor.
 Zhang Z, Zhou Y;
 (GETH) GENENTECH INC.
 WPI; 2004-347921/32.
P-PSDB; ABM82223.
 Percent Similarity:
Best Local Similarity:
 Alignment Scores:
 26-FEB-2004
```

88

```
This represents the nucleotide sequence of the plasmid construct used for the expression of human heart O-fucosyltransferase. The human O-fucosyltransferase can glycosylate an epidermal growth factor (EGF) domain of a polypeptide with an activated O-fucose residue. Inhibitors of O-fucosyltransferase, e.g. mutents with increased affinity for the EFG domains, are used in diagnosis and treatment of conditions associated with overexpression of O-fucosyltransferases, to promote survival of sensory (retinal) neurons. Probes based on EGF domain polypeptide are used to detect gene amplification and expression. The expression can also be determined at the protein level using antibodies specific for O-
 Human O-fucosyl:transferase able to glycosylate epidermal growth factor domains - useful for diagnosis and treatment of diseases involving
 1440. 5333
**tag= a
/note= "insert coding for human O-fucosyltransferase."
 4302 AACCAGGCCGATCACTTCTTGGGCTCTCTGGCATTTGCAAAGCTGCTAAACCGTACCTTG
 AlaglySerTrpAspLeuAlaGlyTyrLeuLeuTyr***Pro***MetGlyArgPheGly
 23 AsnGlnAlaAspHisPheLeuGlySerLeuAlaPheAlaLysLeu***ValArgThrLeu
 43 AlaValProProTrpIleGluTyrGlnHisHisLysProProPheThrAsnLeuHis
 O-fucosyltransferase; epidermal growth factor; EGF; glycosylation; O-fucose; inhibitor; sensory neuron; retinal neuron; human; heart;
 Sequence 11284 BP; 2947 A; 2602 C; 2624 G; 3111 T; 0 U; 0 Other;
 Length:
Matches:
Conservative:
 Mismatches:
 /note= "polyhistidine tag"
 Indels:
 US-09-774-954-3 (1-61) x AAV65633 (1-11284)
 ocation/Qualifiers
 Example; Page 49-57; 90pp; English
 97US-00792498.
 7.63e-32
295.00
91.53%
91.53%
 overexpression of the enzyme
 97WO-US023401
 .4235
 /note= '4218. .
 /*tag=
 (GETH) GENENTECH INC.
 Spellman MW;
 WPI; 1998-437477/37.
P-PSDB; AAW80573.
 fucosyltransferase
 Percent Similarity:
Best Local Similarity:
 Homo sapiens.
Synthetic.
 17-DEC-1997;
 31-JAN-1997;
 26-NOV-1997;
 misc_feature
 Alignment Scores:
 WO9833924-A1
 06-AUG-1998
 4362
 Wang Y,
 Query Match
 ..
No.:
셤
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 257
 ecesecrecreseaccesecestracerecretracrececerecareseseseserrings 197
 The present invention relates to a method (M1) for determining the subtype of leukaemia cells and whether a patient sample contains leukaemia cells. The method comprises determining the expression profile of a group of markers in a patient sample. The method is useful for determining the presence of leukaemia cells, its types or subtypes, and for the preparation of a medicament for treating leukaemia.
 52
 AsnGlnAlaAspHisPheLeuGlySerLeuAlaPheAlaLysLeu***ValArgThrLeu 42
 Determining the subtype of leukemia cells and whether a patient sample contains leukemia cells or other cells, useful for treating leukemia, comprises determining the expression profile of a group of markers in a
 Dugas M;
 198 AACCAGGCCGATCACTTCTTGGCTCTCTGGCATTTGCAAAGCTGCTAAACCGTACCTTG
 3 AlaGlySerTrpAspLeuAlaGlyTyrLeuLeuTyr***Pro***MetGlyArgPheGly
 AlaValProProTrpIleGluTyrGlnHisHisLysProProPheThrAsnLeuHis 61
 BP; 1280 A; 1278 C; 1331 G; 1346 T; 0 U; 31 Other;
 Plasmid construct for expression of human O-fucosyltransferase.
 Kohlmann A, Schnittger S,
 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
 Disclosure; SEQ ID NO 2310; 2938pp; English
 Cytostatic; Gene therapy; leukaemia; ss.
 US-09-774-954-3 (1-61) x ADF81754 (1-5266)
 Leukaemia-related DNA sequence #2310.
 DEUT KREBSFORSCHUNGSZENTRUM.
UNIV LUDWIG MAXIMILIANS.
HAFERLACH T.
 Brors B, Mergenthaler S;
 Kern W,
 BP
 AAV65633 standard; DNA; 11284
 2.88e-32
295.00
91.53%
91.53%
 04-NOV-2002; 2002WO-EP012303
 2001EP-00126244
2002EP-00009758
 (first entry)
 Schoch C,
 WPI; 2003-505037/47
 Best Local Similarity:
 SCHOCH C.
 WO2003039443-A2
 patient sample.
 KERN W.
 Percent Similarity:
 Sequence 5266
 Haferlach T,
 05-NOV-2001;
30-APR-2002;
 Unidentified
 Alignment Scores:
 16-DEC-1998
 L5-MAY-2003
 23
 43
 258
 AAV65633;
 (HAFE/) I
(SCHO/) (KERN/)
 Eils R,
 DEKR-)
 Query Match:
 Pred. No.:
 AAV65633

1D AAV6

XX AC AAV6

XX AAV6

XX DT 16-I

XX DB Plas
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4361

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AAK52494
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 The invention relates to polymuclectides (AAKS1456-AAKS3435) and the encoded polypeptides (AAM73323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polymeries and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, hematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity tissue growth factor activity, immunomodulatory activity and activity, tissue growth factor activity, immunomodulatory activity and inflammation. Note: Records for SEQ ID NO 2100 (AAKS2581), 2111 inflammation. Note: Records for SEQ ID NO 2100 (AAKS2581), 2111 (AAKS2582) and 3666 (AAM80021) are omitted as the relevant pages from the sequence listing were missing at the time of publication
 Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy.
 Human, cytokine, cell proliferation, cell differentiation, gene therapy, vaccine, peptide therapy, stem cell growth factor, haematopoiesis, tissue growth factor, immunomodulatory, cancer, leukaemia, nervous system disorder, arthritis; inflammation, ss.
 Y;
Wang ZW;
 Seguence 5230 BP; 1285 A; 1255 C; 1330 G; 1360 T; 0 U; 0 Other;
 Drmanac RT, Asundi V, Zhou P, Xu C, Cao Wang D, Wang J, Zhang J, Ren F, Chen R, Wejhrman T, Goodrich R;
 Claim 1; Page 638-642; 6221pp; English.
 Human polynucleotide SEQ ID NO 55.
 03-FEB-2000; 2000US-00496914.
27-AFR-2000; 2000US-00560B75.
20-UIN-2000; 2000US-00590075.
19-UIL-2000; 2000US-00654936.
15-SEP-2000; 2000US-00654936.
20-CT-2000; 2000US-0063325.
30-NOV-2000; 2000US-00728422.
 AAK51510 standard; cDNA; 5230
 05-FEB-2001; 2001WO-US004098
 06-NOV-2001 (first entry)
 WPI; 2001-476283/51.
 (HYSE-) HYSEQ INC.
 Tang YT, Liu C,
Ma Y, Zhao QA, ¹
Xue AJ, Yang Y,
 P-PSDB; AAM78377
 WO200157190-A2.
 Homo sapiens
 09-AUG-2001
 AAK51510;
RESULT 5
```

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The invention relates to polymucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polymucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides are useful in gene therapy, vaccines or activity, tisem cell growth factor activity, haematopoiesis regulating activity, tisem cell growth factor activity, immunomodulatory activity and activity, tiseus growth factor activity, immunomodulatory activity and activity, inhibin activity and may be useful in the diagnosis and/or reatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: Records for SEQ ID NO 2110 (AAK55581), 2111 (AAK55582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication
 Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy.
 Human, cytokine, cell proliferation, cell differentiation, gene therapy, vaccine, peptide therapy, stem cell growth factor, haematopoiesis, tissue growth factor, immunomodulatory, cancer; leukaemia, nervous system disorder; arthritis; inflammation, 88.
 Tang YT, Liu C, Drmanac RT, Abundi V, Zhou P, Xu C, Cao Y;
Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
Xue AJ, Yang Y, Wejhrman T, Goodrich R;
 Sequence 4850 BP; 1142 A; 1218 C; 1244 G; 1246 T; 0 U; 0 Other;
 Claim 1; Page 4424-4425; 6221pp; English.
 Human polynucleotide SEQ ID NO 2023
 AAK52494 standard; cDNA; 4850 BP.
 03-FEB-2000; 2000US-00496914.
27-APR-2000; 2000US-00560875.
20-UTW-2000; 2000US-0059075.
19-UTW-2000; 2000US-0063025.
01-SEP-2000; 2000US-00654936.
15-SEP-2000; 2000US-00654936.
20-OCT-2000; 2000US-0063325.
 05-FEB-2001; 2001WO-US004098
 (first entry)
 WPI; 2001-476283/51.
P-PSDB; AAM79361.
 (HYSE-) HYSEQ INC.
 WO200157190-A2.
 Homo sapiens.
 09-AUG-2001.
 06-NOV-2001
 AAK52494;
```

21

7 AspLeuAlaGlyTyrLeuLeuTyr\*\*\*Pro\*\*\*Met---------GlyArgPhe

US-09-774-954-3 (1-61) x AAK51510 (1-5230)

5230 44 4 7 7 5

Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:

4.11e-23 232.50 80.00% 73.33%

> Percent Similarity: Best Local Similarity:

Best Local Si Query Match: DB:

Alignment Scores: Pred. No.: Conservative: Mismatches: Indels:

Percent Similarity: Best Local Similarity:

Alignment Scores:

Pred. No.:

Score:

Length: Matches:

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This represents a first EcoR1 nucleotide fragment of human KIAA0180. This 5009 basepairs partial cDNA encodes for a protein of unknown function from myeblast celline KG-1. The invention provides a human heart Ofucosyltransferase that can glycosylate an epidermal growth factor (EGF) domain of a polypeptide with an activated Ofucose residue. Inhibitors of Ofucosyltransferase, e.g. mutants with increased affinity for the EFG domains, are used in diagnosis and treatment of conditions associated with overexpression of Ofucosyltransferase, to promote survival of sensory (retinal) neurons. Probes based on EGF domain polypeptide are used to detect gene amplification and expression. The expression can also be determined at the protein level using antibodies specific for O
 220 GGGAACCAGGCCGATCACTTCTTGGCCTCTCTGGCATTTGCAAAGCTGCTGAACCGTTCC 279
 280 Trescrictic criterresarrisas raccas carcacaas cerecriticas caas cricar 339
 21
 61
 22 GlyAsnGlnAlaAspHisPheLeuGlySerLeuAlaPheAlaLysLeu***ValArgThr 41
 factor
 O-fucosyltransferase; epidermal growth factor; EGF; glycosylation;
O-fucose; inhibitor; sensory neuron; retinal neuron; human; heart; ss.
 42 LeuAlaValProProTrpIleGluTyrGlnHisHisLysProProPheThrAsnLeuHis
 Human O-fucosyl:transferase able to glycosylate epidermal growth f. domains - useful for diagnosis and treatment of diseases involving
 4850
42
5
8
8
1
 7 AspleuAlaGlyTyrLeuLeuTyr***Pro***Met-----
 First EcoR1 nucleotide fragment of human KIAA0180
 Length:
Matches:
Conservative:
Mismatches:
Indels:
 Gaps:
 US-09-774-954-3 (1-61) x AAK52494 (1-4850)
 Example 1; Fig 11; 90pp; English.
 BP
 AAV65634 standard; cDNA; 5009
 97US-00792498.
 97WO-US023401
 overexpression of the enzyme
 2.14e-21
220.50
78.33$
70.00$
 (first entry)
 (GETH) GENENTECH INC.
 Spellman MW
 WPI; 1998-437477/37.
P-PSDB; AAW80577.
 Best Local Similarity:
Query Match:
 Percent Similarity:
 Homo sapiens.
 WO9833924-A1.
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26-NOV-1997;
 17-DEC-1997;
Alignment Scores:
Pred. No.:
 16-DEC-1998
 06-AUG-1998
 Wang Y,
 RESULT 7
AAV65634
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Sequence 5009 BP; 1235 A; 1195 C; 1268 G; 1311 T; 0 U; 0 Other;

fucosyltransferase

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18
 61
 The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins (ABBC) ABBC) ABBCO). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.
 62 GCTGTCCCTCCTTGGATTGAGTACCAGCATCACAAGCCTCCTTTCACCAACCTCCAT 118
 23 AsnGlnAlaAspHisPheLeuGlySerLeuAlaPheAlaLysLeu***ValArgThrLeu
 2 AACCAGGCCGAICACTICTIGGGCTCTCTGGCAITTGCAAAGCTGCTAAACCGTACCTTG
 61
 43 AlaValProProTrpIleGluTyrGlnHisHisLysProProPheThrAsnLeuHis
 Drosophila melanogaster expressed polynucleotide SEQ ID NO 36323
 Drosophila; developmental biology; cell signalling; insecticide;
 BP; 302 A; 313 C; 307 G; 287 T; 0 U; 0 Other;
 Claim 1; SEQ ID NO 36323; 21pp + Sequence Listing; English.
 1209
33
3
 Conservative:
 Length:
Matches:
 Œ.
 Gaps:
 US-09-774-954-3 (1-61) x AAV65634 (1-5009)
 Myers
 ABL13947 standard; cDNA; 1209 BP
 PWD,
 23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
 23-MAR-2001; 2001WO-US009231
5.84e-19
204.00
94.87%
94.87%
 8.6e-16
177.00
80.00%
 (first entry)
 ij
 pharmaceutical; gene; ss
 Drosophila melanogaster.
 Venter JC, Adams M,
 WPI; 2001-656860/75
 (PEKE) PE CORP NY
 P-PSDB; ABB69844.
 WO200171042-A2.
 Score:
Percent Similarity:
 Sequence 1209
 Alignment Scores:
Pred. No.:
 26-MAR-2002
 27-SEP-2001.
 ABL13947;
 Query Match:
DB:
 ABL13947
 RESULT
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 The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and insecticides in the inspect entaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16175) and the encoded proteins (ABB57737) as ABB72072). The sequence data for this gatent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 141
 56
 New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.
 Drosophila melanogaster expressed polynucleotide SEQ ID NO 36320.
 Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical; gene; ss.
 Sequence 3264 BP; 904 A; 742 C; 758 G; 860 T; 0 U; 0 Other;
 Claim 1; SEQ ID NO 36320; 21pp + Sequence Listing; English.
 Length:
Matches:
Conservative:
Mismatches:
000
Mismatches:
Indels:
Gaps:
 Li PWD, Myers EW;
 US-09-774-954-3 (1-61) x ABL13947 (1-1209)
 ABL13946/c
ID ABL13946 standard; cDNA; 3264 BP.
 1.49e-10
145.00
87.88%
78.79%
 23-MAR-2000; 2000US-0191637P.
 23-MAR-2001; 2001WO-US009231.
 47 TrplleGluTyrGln 51
|||:::|||||:::
202 TGGGTGGAGTATCGT 216
 26-MAR-2002 (first entry)
 73.33$ 54.29$
 Drosophila melanogaster.
 Venter JC, Adams M,
 WPI; 2001-656860/75.
P-PSDB; ABB69843.
 (PEKE) PE CORP NY.
Best Local Similarity:
Query Match:
DB:
 WO200171042-A2.
 Alignment Scores:
Pred. No.:
 27-SEP-2001.
 ABL13946;
 RESULT 9
 g
 g
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Score: Percent Similarity: Rest Local Similarity:

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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryces for the development of discloses genomic DNA sequences (ABLIG176-ABL30511), expressed DNA sequences (ABLIG176-ABL30511), expressed DNA sequences (ABLIG175) and the encoded proteins (ABBS7737-ABB72072). The sequence data for this patent did not form part of princed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 2092 GGACGCTTTGGCAACCAGGCCGACCACTTCCTGGGATCATTGGCCTTCGCCAAGGCGCTT 2033
 19 GlyArgPheGlyAsnGlnAlaAspHisPheLeuGlySerLeuAlaPheAlaLysLeu*** 38
 New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.
 Drosophila melanogaster expressed polynucleotide SEQ ID NO 36164.
 Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical; gene; ss.
 Seguence 3793 BP; 1020 A; 853 C; 950 G; 970 T; 0 U; 0 Other;
 Claim 1; SEQ ID NO 36164; 21pp + Sequence Listing; English.
 3793
26
3
4
0
0
 00
 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
 Myers EW;
 US-09-774-954-3 (1-61) x ABL13894 (1-3793)
 US-09-774-954-3 (1-61) x ABL13946 (1-3264)
 ABL13894/c
ID ABL13894 standard; cDNA; 3793 BP.
 Li PWD,
 1.81e-10
145.00
87.88%
78.79%
 23-MAR-2001; 2001WO-US009231
 23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
 (first entry)
 44.48%
 Drosophila melanogaster.
 Venter JC, Adams M,
 WPI; 2001-656860/75.
P-PSDB; ABB69791.
 Percent Similarity:
Best Local Similarity:
Query Match:
DB:
 (PEKE) PE CORP NY.
 WO200171042-A2.
 Alignment Scores:
Pred. No.:
 26-MAR-2002
 27-SEP-2001
 ABL13894;
 Query Match:
DB:
```

ribozyme therapeutics, for detecting related sequences or genetic

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88888888888
 human signal peptide-containing proteins HSPP-1 to HSPP-134. HSPPs have human signal peptide-containing proteins HSPP-1 to HSPP-134. HSPPs have anticancer, anti-inflammatory, antimicrobial, noctropic, hepatotropic, concurrence anticancer, and can be used in open therapy. HSPPs can be used in gene therapy. HSPPs can be used to treat or prevent disorders associated with decreased activity or function of HSPP. Antagonists of HSPP are used to treat or prevent disorders associated with increased activity or function of HSPP. Such diseases include cell proliferation (including cancer), inflammation, cardiovascular, neurological, cirrhosis, psoriasis acquired immune deficiency syndrome, anaemia, asthma, Crohn's disease, microbial or other infections, congestive or ischaemic heart disease, altheimer's, Parkinson's or Huntington's classes, schizophrenia, ovulatory defects, muscular dystrophy). HSPP nucleic acids can be used for the recombinant production of HSPP, for detecting HSPP in a standard hybridisation and mplification assays (for incledic acids can be used for the recombinant production of HSPP, for detecting HSPP in the production of HSPP, for the force of
 diagnosis and monitoring), in gene therapy, as antisense, triplex-forming
 584 GGACGCTTTGGCAACCAGGCCGACCACTTCCTGGGATCATTGGCCTTCGCCAAGGCGCTT 525
 Human; signal peptide-containing protein; HSPP; diagnosis; cancer; inflammation; cardiovascular disease; anticancer; anti-inflammatory; antimicrobial; noctropic; antimicrobial; hepatotropic; antiathmatic; gene therapy; cell proliferation; neurological disorder; reproductive disorder; developmental disorder; arteriosclerosis; cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia; asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia; Parkinson's disease; Huntington's diseases; ovulatory defect;
 New human signal peptide-containing proteins useful in treatment, prevention and diagnosis of e.g. cancer, inflammation and cardiovascular disease.
GlyArgPheGlyAsnGlnAlaAspHisPheLeuGlySerLeuAlaPheAlaLysLeu*** 38
 Corley NC, Guegler KJ, Baughn MR;
H, Patterson C, Reddy R, Hillman JL;
 Human signal peptide containing protein HSPP-102 cDNA SEQ ID NO:236.
 524 AATCGCACCCTGATCCTGCCGCGTGGGTGGAGTATCGT 486
 39 ValArgThrLeuAlaValProProTrpIleGluTyrGln 51
 Claim 9; Page 307; 327pp; English.
 AAZ98210 standard; cDNA; 760 BP
 Gorgone GA,
 98US-0094983P.
98US-0102686P.
 98US-0112129P
 99WO-US014484
 Lal P, Tang YT, Gorgone (
Akerblom IE, Au-Young J,
 (first entry)
 (INCY-) INCYTE PHARM INC
 muscular dystrophy; ss
 WPI; 2000-160673/14.
P-PSDB; AAY87325.
 WO200000610-A2
 Homo sapiens.
 25-JUN-1999;
 11-DEC-1998;
 26-JUN-1998
 31-JUL-1998
 11-MAY-2000
 06-JAN-2000
 01-OCT-1998
 Bandman O;
 AAZ98210;
 RESULT 11
 AAZ98210
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variations, and for chromosomal mapping. HSPP are also used to raise specific antibodies (Ab) and to screen for agonists and antagonists (Dotential therspeutic agents). Ab are used to diagnose, or monitor, HSPP -ralated diseases (in usual immunoassays), as therspeutic antagonists, in competitive drug screens, and for purification of HSPP from natural
 screening
 The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibite proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense polypeptide or its fragment whose expression is inhibited by the antisense mucleic acid; (3) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding
 Zyskind JW;
Xu HH;
 New antisense nucleic acids, useful for identifying proteins or scre
for homologous nucleic acids required for cellular proliferation to
isolate candidate molecules for rational drug discovery programs.
 ds; prokaryotic essential gene; cell proliferation;
 Sequence 760 BP; 171 A; 206 C; 220 G; 163 T; 0 U; 0 Other;
 Äξ
 Ohlsen Forsyth
 Conservative:
Mismatches:
 Haselbeck R,
 Yamamoto R,
 Length:
Matches:
 Claim 14; SEQ ID NO 25606; 1766pp; English.
 Indels:
 US-09-774-954-3 (1-61) x AAZ98210 (1-760)
 Prokaryotic essential gene #19393.
 ACA37736 standard; DNA; 594 BP
 Malone C,
 Carr GJ,
 21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-0094893.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
 21-MAR-2002; 2002WO-US009107
 0.3
76.00
83.33%
77.78%
 (first entry)
 (ELIT-) ELITRA PHARM INC.
 Zamudio C,
Trawick JD,
 WPI; 2003-029926/02.
P-PSDB; ABU33866.
 Mycobacterium avium.
 Percent Similarity:
Best Local Similarity:
Query Match:
 drug design; gene
 WO200277183-A2.
 Alignment Scores:
 19-JUN-2003
 03-OCT-2002
 Antisense;
 ACA37736;
 Wang L,
Wall D,
 Pred. No.:
 RESULT 12
 ACA3773
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the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the strains; or (13) identifying the target of a compound that inhibits the cardins or an organism. The antisense nucleic acids required for proliferation to isolate candidate molecules for rational density proteins or screening for homologous nucleic acids required for proliferation in cells other than S. aurens, S. typhimum.ium, required for proliferation in cells other than S. aurens, S. typhimum.ium, comparate of the printed specification, but was obtained in celectronic format directly from WIPO at Equences
 Non-naturally occurring peptide; anion pump protein; tuberculosis; hypersensitivity reaction; tuberculostatic; gene; ds.
 Sequence 594 BP; 67 A; 204 C; 238 G; 85 T; 0 U; 0 Other;
 406 GTGCGCGCGGTGTTCATCCGCGCGCCCTGGGTGGAG 441
 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
 41 ThrLeuAlaVal ------ProProTrp1leGlu 49
 US-09-774-954-3 (1-61) x ACA37736 (1-594)
 (GENO-) GENOME THERAPEUTICS CORP.
 ADB74382 standard; DNA; 42325 BP
 93US-00109181.
93US-00142558.
 Mycobacterium leprae DNA #16.
 94US-00311731
 (first entry)
 1.96
69.50
56.25%
50.00%
21.32%
 Mycobacterium leprae
 WPI; 2003-656441/62
 Percent Similarity:
Best Local Similarity:
 Мао Ј;
 16-SEP-1994;
 19-AUG-1993;
22-OCT-1993;
 Alignment Scores:
Pred. No.:
 04-DEC-2003
 US6583266-B1
 24-JUN-2003
 Smith DR,
 ADB74382;
 Query Match:
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The invention relates to a non-naturally occurring peptide of
Mycobacterium tuberculosis comprising an amino acid sequence
corresponding to an anion pump protein. The invention also relates to a
corresponding to an anion pump protein. The invention as relates to a
corresponding to an anion pump protein. The invention as a vaccine against Mycobacterium leprae. The new peptide is
useful as a vaccine against Mycobacterium leprae. The new peptide is
cuseful as a vaccine against Mycobacterium tuberculosis or Mycobacterium
cuseful as a vaccine against Mycobacterium tuberculosis or Mycobacterium
cuseful as a vaccine against Mycobacterium tuberculosis or Mycobacterium
corresponse. The peptide may also be used to detect hypersensitivity reactions of individuals exposed to Mycobacterium tuberculosis or
cactions of individuals exposed to Mycobacterium tuberculosis or
mycobacterium leprae. The proteins and peptides may be affixed to solid
supports to detect antibodies typical of hypersensitivity reactions, from
a patient's sera. This sequence represents Mycobacterium leprae DNA of
the invention. Note: The sequence data for this patent did not form part
cof the printed specification but was obtained in electronic format
cof the printed specification but was obtained in electronic format
 30298 TCCTGGGATCTGCGTAAATTC---CTCTGGGCGCGGAGGTGGGCTGCTACGGCATCCAA 30242
 30241 cecarricacrecrécecaacergargararrisecececececesagageseceiries 30182
 toxic effect, gene expression profile; hepatotoxicity; diagnostic marker; toxicity marker; toxicity progression; drug screening; primary rat hepatocyte toxicity modelling; gene; ds.
 5 SerTrpAspLeuAlaGlyTyrLeuLeuTyr***Pro***MetGlyArgPheGlyAsnGln 24
 32 LeuAlaPheAlaLysLeu***ValArgThrLeuAlaValProProTrplleGluTyrGln 51
 -----GlySer 31
 Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3776.
 Sequence 42325 BP; 9673 A; 13128 C; 11330 G; 8194 T; 0 U; 0 Other;
 New Mycobacterium tuberculosis anion pump peptide useful for as tuberculosis vaccine and diagnosis of tuberculosis infection.
 Length:
Matches:
Conservative:
Mismatches:
Indels:
 Disclosure; SEQ ID NO 131; 26pp; English.
 25 AlaAspHisPheLeu-------
 Gaps:
 30148 -----GAGCCGTTCTTTGCCAAC 30131
 US-09-774-954-3 (1-61) x ADB74382 (1-42325)
 52 HisHisLysProProPheThrAsn 59
 ADB53234 standard; DNA; 2720 BP
 04-FEB-2003; 2003WO-US003482
 (first entry)
 68.50
42.65%
33.82%
21.01%
 Percent Similarity:
Best Local Similarity:
Query Match:
 Rattus norvegicus
 WO2003065993-A2.
 Alignment Scores:
 04-DEC-2003
 ADB53234;
 RESULT 14
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1077 Trigarcedegreeretritatarrecaacaecerrrereritreaaatareegaaerrae 1136
 This invention describes novel isolated Streptococcus pneumoniae polynucleotides (see AAZ96173-Z96494) and their encoded proteins (see AAZ96173-Z96494) and their encoded proteins (see AAZ96129. The DNA, vectors and host calls described in the method of the invention are useful for the recombinant expression of the polypeptides. The polypeptides are useful for treatment or prevention of disease, or diagnosis of disease related to expression or activity of ench a polypeptide. They can also be used to screen for compounds which interact with and inhibit or activate such a polypeptide. The polypeptide or DNA encoding them, via gene therapy) are also useful for inducing an immunological response in a mammal. The antagonists are useful to inhibit such bacterial polypeptides. The polypeptides are particularly useful to determine their role in pathogenesis of
::: ||||||
872 GTGCTGGACCCTGAGGTGGACAGTCTCACGCCTTGGCAGCACTTAGTCCTACATGACTGG 931
 Streptococcus pneumoniae proteins and related DNA - useful for screening compounds for antibacterial activity.
 8 LeuAlaGlyTyrLeuLeuTyr***Pro***MetGlyArgPheGlyAsnGlnAlaAspHis 27
 Treatment; prevention; disease; diagnosis; gene therapy; screening; bacterial; antimicrobial; antibiotic; pathogenesis; infection; ss.
 Knowles DJC, Lonetto MA, Nicholas RO;
 Sequence 1660 BP; 467 A; 332 C; 379 G; 479 T; 0 U; 3 Other;
 932 ATGTCAGAGGÁGTÁCTCCCÁCCTGGAGGACCCCGTTÍCTCAAGCTG 976
 ----IleGluTyrGlnHisHisLysProProPheThrAsnLeu
 Conservative:
Mismatches:
 Length:
Matches:
 Indels:
 S. pneumoniae derived DNA from ORF #157.
 Claim 4; Page 191-192; 640pp; English.
 US-09-774-954-3 (1-61) x AAZ96329 (1-1660)
 infection, dysfunction and disease
 (SMIK) SMITHKLINE BEECHAM CORP.
 96US-0024022P.
 AAZ96329 standard; DNA; 1660
 97WO-US014436
 20.1
66.50
48.84%
37.21%
20.40%
 (first entry)
 Streptococcus pneumoniae
 Hodgson JE,
 WPI; 1998-159452/14.
 Similarity:
 P-PSDB; AAY85984
 Percent Similarity:
 10-APR-2000
 15-AUG-1997;
 16-AUG-1996;
 WO9806734-A1
 Alignment Scores:
 19-FEB-1998.
 Stodola RK;
 Black MT,
 AAZ96329
 Query Match
 Best Local
 RESULT 15
 AAZ96329
 Score:
 8
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 The present invention describes a method for determining whether a compound induces a toxic effect on a tissue or cell. The method comprises preparing a gene expression profile of a tissue or cell sample exposed to the compound, and comparing the gene expression profile to a database comprising data or information on the Tox mean and non-Tox mean value. The method is useful for predicting or identifying at least one toxic effect, particularly hepatotoxicity, of a test or unknown compound. The genes listed in the specification are useful as diagnostic or toxicity markers for the prediction or identification of the physiological state of tissue or cell sample that has been exposed to a compound, or to identify or predict the toxic effects of a compound or an agent. These may also be used as markers for monitoring toxicity progression or for
 Determining if a compound induces a toxic effect on a tissue or cell, for identifying hepatotoxic compounds, comprises comparing a gene expression profile of a tissue or cell sample to a database of Tox mean and non-Tox
 811
 751
 GCTTTCATCCAGCCTGAGATGCATACCACCCTGGCCCCTGTGTTCCGAATCTCCCTGCCA 871
 7
 40
 43
 47
 drug screening. The present sequence represents a primary rat hepatocyte toxicity modelling related gene sequence from the present invention.
 GETAACCAGATGGGACAGTATGCCACATTGCTGGCCCTAGCCCAGCTCAATGGCCGG
 LeuAlaGlySerTrpAspLeuAlaGlyTyrLeuLeuTyr***Pro***MetGlyArgPhe
 GlyAsnGlnAlaAspHisPheLeuGlySerLeuAlaPheAlaLysLeu***ValArg---
 Ë
 Orr
 Sequence 2720 BP; 624 A; 719 C; 725 G; 652 T; 0 U; 0 Other;
 Castle A,
 2720
26
7
19
43
 -----ValProProTrp-----
 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
 Higgs B,
 Claim 44; SEQ ID NO 3776; 874pp; English
 US-09-774-954-3 (1-61) x ADB53234 (1-2720)
 Porter M, Johnson K,
 crcrccccacrrccacarc-
 2002US-0371150P.
 2002US-0373602P
 2002US-0374139P
 2002US-0378652P
 2002US-0378653P
 2002US-0378665P
 2002US-0394253P
 2003US-0442900P
 2002US-0373601P
 2002US-0378370P
 2002US-0394230P
 2002US-0407688P
 26.9
67.50
34.74%
27.37%
20.71%
 LOGIC INC.
 WPI; 2003-731472/69.
 Best Local Similarity:
 Percent Similarity:
 10-APR-2002;
11-APR-2002;
19-APR-2002;
 22-APR-2002;
 28-JAN-2003;
 GENE
 Alignment Scores:
 19-APR-2002;
 09-MAY-2002;
 09-MAY-2002;
 09-MAY-2002;
 mean values.
 Mendrick D,
Elashoff M;
 08-APR-2002;
 .0-APR-2002;
 08-MAY-2002;
 04-SEP-2002
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 Query Match:
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<sup>48</sup> IleGluTyr 50 | | | | 1188 TCTGTTTAC 1196

Search completed: October 26, 2005, 09:51:41 Job time : 185.85 secs

protein

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Run on:

Sequence:

Searched:

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AF75884 Homo sapien
AF75884 Homo sapi
AF780153 Sequence
BD103190 O-fucosyl
AY344581 Bos tauru
AY34580 Bos tauru
AY367917 Sus scrot
AY719585 Gallus ga
AY719585 Gallus ga
AY720352 Gallus ga
AY720352 Gallus ga
AY720352 Gallus ga
AY78159 Kenopus L
AY78159 Tetraodon
AY781504 Tetraodon
AY781504 Tetraodon
AY781504 Tetraodon
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AY781504 Tetraodon
AY781504 Tetraodon
AY781504 Tetraodon
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AY781504 Tetraodon
AY781504 Tetraodon
AY781504 Tetraodon
AY781504 Musan DNA
 AF375885 1302 bp mRNA linear ROD 23-OCT-2001
Mus musculus protein o-fucosyltransferase (Pofut1) mRNA, complete
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. 1 (bases 1 to 1302)
Wang, Y.; Shao, L., Shi, S., Harris, R.J., Spellman, M.W., Stanley, P. and Haltiwanger, R.S.
Modification of epidermal growth factor-like repeats with O-fucose. Molecular cloning and expression of a novel GDP-fucose protein
 AY118651 Drosophil
ARS09393 Sequence
AB093572 Drosophil
AJ781502 Ciona sav
 AC094844 Rattus no
AC134371 Rattus no
 BD103189 O-fucosyl
AR163451 Sequence
BD103188 O-fucosyl
 BC000582 Homo sapi
AL832023 Homo sapi
D80002 Homo sapien
 AR163453 Sequence
BD103191 O-fucosyl
 Drosophil
 AJ781500 Pan trogl
AR163452 Sequence
 οĘ
 Sequence
 2 (bases 1 to 1302)
Shi,S., Stanley,P., Wang,Y., Shao,L., Harris,R.J., Spellman,M.W.
and Haltiwanger,R.S.
 Direct Submission
Submitted (02-MAY-2001) Cell Biology, Albert Einstein College
Medicine, 1300 Morris Park Ave., New York, NY 10461, USA
Location/Qualifiers
 AJ831490 I
 O-fucosyltransferase
J. Biol. Chem. 276 (43), 40338-40345 (2001)
21523965
 ALIGNMENTS
 SSC567917
A7781503
A7781503
A7719585
GGA535754
BC082519
A7720352
BC082519
A7781498
A7781498
A7781504
A7781504
A7781504
A7781504
A7781504
A7781504
A7781504
 BC000582
HSM803330
 AY344581
AY344580
 AL807380
 AC094844
AC134371
AR163453
BD103191
AJ81490
CQ590403
AZ118651
AK5093572
AJ781502
AJ781501
AK112708
BD103196
CQ727777
AJ781500
AR163452
BD103189
AR163451
BD103188
 AX780153
BD103190
 AF375884
 Mus musculus (house mouse)
 AF375885.1 GI:15825115
 240336
240510
 5009
5009
1209
1209
1295
1320
 208614
 Mus musculus
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 October 26, 2005, 05:08:04; Search time 1382.21 Seconds (without alignments) 2138.440 Million cell updates/sec
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
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Email: capabs.r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.

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CDNA Library Arrayed by: The I.M.A.G.E. Consortium

CDNA Library Arrayed by: The I.M.A.G.E. Consortium

CDNA Sequencing Center (NISC)

Gathersburg, Maryland;

Web site: http://www.nisc.nih.gov/

CONTECT: nisc mgceMhgri.nih.gov/

CONTECT: nisc mgceMhgri.nih.gov/

CONTECT: nisc mgceMhgri.nih.gov/

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Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 Strausberg, R.
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Submitted (31-JAN-2003) National Institutes of Health, Mammalian Submitted (31-JAN-2003) Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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 A new superfamily of protein-O-fucosyltransferases, alpha2-fucosyltransferases: and alpha6-fucosyltransferases: phylogeny and identification of conserved peptide motifs Glycobiology 13 (12), 1C-5C (2003)
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 Martinez-Duncker, I., Mollicone, R., Candelier, J.J., Breton, C. Oriol, R.
A new superfamily of protein-O-fucosyltransferases, alpha2-fucosyltransferases, and alpha6-fucosyltransferases: phylogeny and identification of conserved peptide motifs phycology 13 (12), 1C-5C (2003)
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NG WANG, MICHAEL W SPELLMAN

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Nang, Y. and Spellman, W.W.

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Patent: JP 2001527389-A 9 25-DEC-2001;

GENENTECH INC

SUMMOGNITHEN

DP 2-DEC-2001

PP 17-DEC-1997 JP 1998532877

PR 31-JAN-1997 US 08/792498,26-NOV-1:

PR 17-DEC-1997 US 08/792498,26-NOV-1:

PR 31-JAN-1997 US 08/792498,26-NOV-1:

PR 31-JAN-1997 US 08/792498,26-NOV-1:

CC Strandedness: Single;

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CC O-fucosyltransferase

CC O-fucosyltransferase

FF Key

L. 1100

FT SOURCE

CC O-fucosyltransferase

FF F SOURCE

CC O-fucosyltransferase

CC O-fucosyltransferase

FF F SOURCE

CC O-fucosyltransferase

L. 1100

FT CO-fucosyltransferase

CC O-fucosyltransferase

CC O-fucosyltransferase

CC O-fucosyltransferase

FF F SOURCE

CC O-fucosyltransferase

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ORGANISM
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PAT 17-0CT-2001
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Wang, Y. and Spellman, M.W.
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Patent: JP 201527389-A 2 25-DEC-2001;
GENENTECH INC
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OS Unidentified
PN JP 2001527389-A/2
PP 17-DEC-1997 JP 1998532877
PR 31-JAN-1997 US 08/792498, 26-NOV-1
YANG WANG, MICHAEL W SPELLMAN
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DEFINITION

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Pred. No.:

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AUTHORS TITLE JOURNAL FEATURES

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Score:

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Wangy, and Spellman, W.W.

O-fucosyltransferase
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GENEWATECH INC
GENEWATECH INC
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PP 25-DEC-1907 Up 1998532877
PR 31-JAN-1997 US 08/792498, 26-NOV-1997 US
YANG WANG, MICHELL W SPELLMAN
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Unclassified.
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91.53%
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Neuherberg, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DFF2); Email S. Wiemann@dkfz-heidelberg.de;
sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing
consortium of the German Genome Project.
This clone (DKF2P45JJ114) is available at the RZPD in Berlin.
Please conteat the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERWANY; Email: clone@rzpd.de Further
information about the clone and the sequencing project is available
at http://mips.gsf.de/proj/cDNA/.
 PRI 10-JAN-2003
 57 GCGGGCTCCTGGGACCCGGTTACCTGCTCTACTGCCCCTGCATGGGGCGCTTTGGG 116
 117 AACCAGGCCGATCACTTCTTGGGCTCTCTGGCATTTGCAAAGCTGCTAAACCGTACCTTG 176
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 23 AsnGlnAlaAspHisPheLeuGlySerLeuAlaPheAlaLysLeu***ValArgThrLeu 42
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Contact: nisc_mgc@nhgrl.nih.gov/
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Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,B.D.
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Mangy, Y., Shao, L., Shi, S., Harris, R.J., Spellman, M.W., Stanley, P.
Mangy, Y., Shao, L., Shi, S., Harris, R.J., Spellman, M.W., Stanley, P.
and Haltiwanger, R.S.
Modification of epidermal growth factor-like repeats with O-fucose.
Modification of epidermal growth factor-like repeats with O-fucose.
Modification of epidermal growth factor-like repeats with O-fucose.
O-fucosyltransferase
J. Biol. Chem. 276 (43), 40338-40345 (2001)
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Shi,S., Stanley,P., Wang,Y., Shao,L., Harris,R.J., Spellman,M.W.
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Submitted (02-MAY-2001) Cell Biology, Albert Einstein College of Medicine, 1300 Morris Park Ave., New York, NY 10461, USA
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 Chiang, P.W., Wang, S., Smithivas, P., Song, W.J., Ramamoorthy, S., Hillman, J., Puett, S., Van Keuren, M.L., Crombez, E., Kunar, A., Glover, T.W., Miller, D.E., Tsai, C.H., Blackburn, C.C., Chen, X.N., Sun, Z., Cheng, J.F., Korenberg, J.R. and Kurnit, D.W. Indentification and analysis of the human and murine putative chematin structure regulator SUPTGH and Supt6h
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Mismatches:
Indels:
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Best Local Similarity:
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 COMMENT
FEATURES
SOURCE
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MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
 JOURNAL
MEDLINE
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AUTHORS
 gene
 PUBMED
 CDS
 TITLE
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Search completed: October 26, 2005, 12:55:28 Job time : 1386.21 secs

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| 5.1.6   | Compugen  |
| version | - 2005    |
| enCore  | 1993      |
| Ger     | ΰ         |
|         | Copyright |

OM protein - protein search, using sw model

October 25, 2005, 15:21:43; Search time 7.64066 Seconds (without alignments) 768.157 Million cell updates/sec Run on:

US-09-774-954-3 326 1 RLAGSWDLAGYLLYXPXMGR.....LAVPPWIEYQHHKPPFTNLH 61 Title: Perfect score: Sequence:

283416 seqs, 96216763 residues Searched:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR\_79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Description         | hypothetical prote | О      | cholesterol oxidas |        | SpoE family protei | divisio | hypothetical prote | n      | galactoside 2-alph | hypothetical prote | hypothetical prote | hypothetical prote | amidotransferase h | >      | ਯ      | hypothetical prote | probable acetyltra | hypothetical prote | hypothetical prote | opsin, green-sensi | amino acid permeas | hypothetical prote | probable phospholi | hypothetical prote | phosphate ABC tran | lipoprotein signal | hypothetical prote | (S) -N-methylcoclau | hypothetical prote |
|---------------------|--------------------|--------|--------------------|--------|--------------------|---------|--------------------|--------|--------------------|--------------------|--------------------|--------------------|--------------------|--------|--------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|---------------------|--------------------|
| ID                  | T15511             | E86957 | S72824             | 151266 | D95101             | E97969  | T40967             | F70736 | A36047             | T21217             | C70570             | S76943             | S72721             | B86968 | AE0875 | T22255             | A75475             | T21655             | T21662             | A42347             | AF0488             | T41004             | T02648             | C69879             | A70127             | AI2377             | F83032             | 796                 | A70199             |
| DB                  | 1                  | 0      |                    |        |                    |         |                    |        |                    |                    |                    |                    |                    | 7      |        |                    |                    |                    |                    |                    |                    |                    |                    |                    |                    | 7                  |                    |                     |                    |
| eng                 | 474                | 569    | 585                | 354    | 767                | 767     | 562                | 578    | 365                | 674                | 198                | 491                | 219                | 223    | 348    | 363                | 207                | 225                | 227                | 322                | 467                | 492                | 514                | 214                | 328                | 158                | 231                | 260                 | 1465               |
| %<br>Query<br>Match | 35.0               | 21.0   | 21.0               | 20.7   | 20.4               | 20.4    | 19.3               | 19.0   | 18.9               | 18.7               | 18.3               | 18.3               | 17.9               | 17.9   | 17.9   | 17.5               | 17.3               | 17.3               | 17.3               | 17.3               | 17.3               | 17.3               | 17.3               | 17.2               | 17.2               | 17.0               |                    | 17.0                | 17.0               |
| Score               | 114                | 68.5   | 68.5               | 67.5   | 66.5               | 66.5    | 63                 | 62     | 61.5               | 61                 | 59.5               | 59.5               | 58.5               | 58.5   | 58.5   | 57                 | 56.5               | 56.5               | 56.5               | 56.5               | 56.5               | 56.5               | 56.5               | 26                 | 26                 | 55.5               | 55.5               | 55.5                | 55.5               |
| Result<br>No.       | -                  | 7      | e                  | 4      | S                  | y       | 7                  | 60     | O                  | 10                 | 11                 | 12                 | 13                 | 14     | 15     | 16                 | 17                 | 18                 | 19                 | 20                 | 21                 | 22                 | 23                 | 24                 | 25                 | 26                 | 27                 | 28                  | 29                 |

| NADH2 dehydrogenas<br>hypothetical prote | NADH2 dehydrogenas | hypothetical prote | probable aminotran | polyketide synthas | NADH2 dehydrogenas | NADH2 dehydrogenas | NADH2 dehydrogenas | NADH dehydrogenase | NADH2 dehydrogenas | ybdS protein - Esc | probable membrane | probable membrane | citrate carrier (i | fructose-bisphosph |
|------------------------------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|-------------------|--------------------|--------------------|
| T12357<br>T27763                         | T13973             | T14795             | AF3342             | T30226             | T17056             | T17059             | T12335             | B90626             | T11076             | B64795             | G85560            | C90710            | AE0578             | PARFAS             |
| 0 0                                      | 7                  | ~                  | ~                  | ~                  | N                  | ~                  | ~                  | 7                  | N                  | Н                  | ~                 | N                 | ~                  | н                  |
| 345<br>428                               | 346                | 383                | 406                | 8563               | 344                | 344                | 344                | 346                | 346                | 487                | 487               | 487               | 501                | 333                |
| 16.9                                     | 16.7               | 16.7               | 16.7               | 16.7               | 16.6               | 16.6               | 16.6               | 16.6               | 16.6               | 16.6               | 16.6              | 16.6              | 16.6               | 16.4               |
|                                          |                    |                    |                    |                    |                    |                    |                    |                    | _                  | _                  |                   |                   |                    |                    |
| 55.5                                     | 54.5               | 54.5               | 54.5               | 54.5               | 54                 | 54                 | 54                 | 54                 | 5                  | Ś                  | 52                | Ň                 | 54                 | 53.5               |

## ALIGNMENTS

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Nature 409, 1007-1101, 2001
A;Authors Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq. A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq. A;Authors: E86909; MUD:21128732; PMID:11234002
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E3.
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 Score 66.5; DE
Pred. No. 1.2;
5; Mismatches
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Best Local Similarity 37.2%;
Matches 16; Conservative
 RESULT 6
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 а
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N.Alternate names: B1620_C3_240 protein
Cispecias: Mycobacterium leprae
Cispecias: Mycobacterium leprae
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R;Register. E.A.; Yokoyama, R.; Yokoyama, S.
A; Tetle: Multiple origins of the green-sensitive opsin genes in fish.
A;Reference number: I51266, MuID:95018302; PMID:7932788
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 5 SWDLAGYLLYXPXMGRFGNQADHFL------GSLAFAKLXVRTLAVPPWIEYQ 51
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 114 --EPFFAN 119
 98 --EPFFAN 103
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Nature: 393, 537-544, 1998
A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Atitle: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:9829897; PMID:9634230
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 359 GSYLIGGYQTYLPKFIETQYGRSASMADIYSGIISVGAIAVST-ALGGWILSRYNIAPRS 417
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----ham 26; Conservative
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A;Gene: CESP:F21G4.1
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418 SI 419
 59 NL 60
 C;Genetics:
A;Gene: Rv2604c
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 C;Accession: A36047
R;Larsen, R.D.; Ernst, L.K.; Nair, R.P.; Lowe, J.B.
R;Larsen, R.D.; Ernst, L.K.; Nair, R.P.; Lowe, J.B.
Aproc. Natl. Acad. Sci. US.A. 87, 6674-6678, 1990
A;Title: Wolecular cloning, sequence, and expression of a human GDP-L-fucose:beta-D-gala A;Reference number: A36047; MUID:90370848; PMID:2118655
 o S
 R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Auture 33, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.B.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; PMID:9634230
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A;Experimental source: strain 972h-; cosmid c1442
B;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Volckaert, G.
submitted to the EMBL Data Library, March 1999
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 ;Cross-references: EMBL:AL049559; PIDN:CAB40185.1; GSPDB:GN00068; SPDB:SPCC1450.18; Experimental source: strain 972h-; cosmid c1450
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C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
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C;Date: 16-Nov-1990 #sequence_revision 16-Nov-1990 #text_change 09-Jul-2004
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 Indels
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A;Accession: T40967
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 5 SWDLAGYLLYXPXMGRFGNQADHFL-
 A; Experimental source: strain H37Rv
 Gene: SPCC1450.18; SPCC1442.02
 A; Molecule type: DNA
 Accession: T41000
 Accession: F70736
 A;Accession: A36047
 A; Map position: 3
 Query Match
Best Local·S
Matches 20
 C;Genetics:
A;Gene: choD
 RESULT 9
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C; Superfamily: conserved hypothetical protein HI1648

Query Match Best Local Si Matches 21

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C;Accession: AE0875
R;Parkhill, J; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, R;Parkhill, J; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica servora, A;Reference number: AB0502; MUID:21534947; PMID:11677608
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C;Species: Mycobacterium leprae
C;Species: Nycobacterium leprae
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: B86968
R;Davies, R.M.; Devlin, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Hor R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd, Baure 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simmonds, M.; Skelton, J.; Squares, R.; Squares, A;Feference number: A86909; MulD:21128732; PMID:11234002
A;Accession: B86908
 A;Scatus: preliminary
A;Molecule type: DNA
A;Residues: 1-223 <SITO>
A;Cross-references: UNIPROT:Q9CCT5; GB:AL450380; NID:g13092704; PIDN:CAC29982.1; GSPDB:GR
 D-erythxose 4-phosphate dehydrogenase [imported] - Salmonella enterica subsp. enterica st
Cispecies; Salmonella enterica subsp. enterica servoar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
 Ä
 7
 A;Accession: AE0875
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1.348 <PAR>
A;Residues: 1.348 <PAR>
A;Residues: GB:AL513382; PIDN:CAD02901.1; PID:g16504154; GSPDB:GN00176
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 Gaps
 2 LAGSWDLAGYLLYXPXMGRFGNQADH-----FLGSLAFAKLXVRTLAVPPWIE 49
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Matches 14; Conservative 4; Mismatches 11; Indels
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Matches 19; Conservative 4; Mismatches 25; Indels
 A,Gene: STY3228
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 A;Gene: ML0474
C;Superfamily: conserved hypothetical protein HI1648
137 FGRQVDSFEGDIGFAGLVDPVRAVFIRAPWVE 168
 21 FGNQADHFLGSLAFAKLX - VRTLAV-PPWIE 49
 Search completed: October 25, 2005, 15:36:43 Job time : 9.64066 secs
 C, Genetics:
 RESULT 15
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 amidoransferase hisH homolog - Mycobacterium leprae
N.Alternate names: B1177 C1 149
C;Species: Mycobacterium leprae
C;Dete: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S72721
R;Smith, D.R.; Robison, K.
R;Smith, D.R.; Robison, K.
A;Description: Mycobacterium leprae cosmid B1177.
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 CiSpecies: Synechocystis sp. (strain PCC 6803)
CiSpecies: Synechocystis sp.
A;Variety: PCC 6803
C;Species: Synechocystis sp.
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S76943
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O, Wumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
 A;Cross-references: UNIPROT:P74735; EMBL:D90917; GB:AB001339; NID:g1653836; PIDN:BAA1885
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
 3,
 7
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 6 WDLAGYLLYXPXMGR-----FGNQADHFLGSLAFAKLXVRTLAVPPWIEYQHHKPP 56
 3 AGSWDLAGYLLYXPXMGR------FGNQADHFLGSLAFAKLX--VRTLAV 44
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 Gaps
 Gaps
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Matches 17; Conservative 9; Mismatches 27; Indels 11;
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A;Accession: S76943
A;Stetus: preliminary
A;Molecule type: DNA
A;Residues: 1-491 <KAN>

: | 148 MSEL 151 57 FTNL 60

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RESULT 13 S72721

A,Gene: hisH C,Superfamily: conserved hypothetical protein H11648

21 FGNQADHFLGSLAFAKLX -- VRTLAV - PPWIE 49

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October 25, 2005, 15:20:23 ; Search time 38.8296 Seconds (without alignments) 607.588 Million cell updates/sec
 61
 US-09-774-954-3
326
1 RLAGSWDLAGYLLYXPXMGR......LAVPPWIEYQHHKPPFTNLH
 2105692
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
 Total number of hits satisfying chosen parameters:
 2105692 seqs, 386760381 residues
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 OM protein - protein search, using sw model
 BLOSUM62
Gapop 10.0 , Gapext 0.5
 geneseqp2002s:*
geneseqp2003as:*
geneseqp2003bs:*
geneseqp2004s:*
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geneseqp1990s:*
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geneseqp2001s:*
 A Geneseq 16Dec04:*
1: geneseqp1980s:*
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Maximum DB seq length: 2000000000
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Perfect score:
 Scoring table:
 Database :
 Sequence:
 Searched:
 Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|            | Description | Aaw80572 N-termina | Aaw80574 N-termina | Aaw80571 Human hea | Abm82223 Tumour-as | Aaw80573 Human O-f | Aam78377 Human pro |          |          |          |          |          | Abu33866 Protein e |          | S. pn    |          | Aau37750 Streptoco |          | Abu45987 Protein e | Aay81596 Streptoco |          | Aar13751 GDP-Fuc:b | Aar45936 A glycosy | 'n       | Aar80154 GDP-L-fuc | Aar70422 2-Alpha-f |
|------------|-------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|----------|----------|----------|----------|----------|--------------------|----------|----------|----------|--------------------|----------|--------------------|--------------------|----------|--------------------|--------------------|----------|--------------------|--------------------|
| SUMMARIES  | ID          | AAW80572           | AAW80574           | AAW80571           | ABM82223           | AAW80573           | AAM78377           | AAM79361 | AAW80577 | ABB63790 | AAW80575 | AAY87325 | ABU33866           | ADK48560 | ABU01274 | ADR94975 | AAU37750           | AAU38005 | ABU45987           | AAY81596           | AAW97416 | AAR13751           | AAR45936           | AAR70421 | AAR80154           | AAR70422           |
| į          | DB.         | ~                  | ~                  | ~                  | 8                  | ~                  | 4                  | 4        | 7        | 4        | N        | ო        | 9                  | ω        | 9        | 80       | 4                  | 4        | 9                  | m                  | ~        | ~                  | 7                  | 7        | ~                  | 7                  |
| 1          | Length      | 61                 | 61                 | 365                | 388                | 397                | 417                | 417      | 343      | 402      | 28       | 150      | 198                | 737      | 741      | 763      | 767                | 767      | 767                | 768                | 783      | 365                | 365                | 365      | 365                | 365                |
| *<br>Ouery | Match       | 98.2               | 90.5               | 90.5               | 90.5               | 90.5               | 71.3               | 67.6     | 62.6     | 54.3     | 24.8     | 23.3     | 21.3               | 20.4     | 20.4     | 20.4     | 20.4               | 20.4     | 20.4               | 20.4               | 20.4     | 18.9               | 18.9               | 18.9     | 18.9               | 18.9               |
| ę          | Score       | 320                | 295                | 295                | 295                | 295                | 232.5              | 220.5    | 204      | . 177    | 81       | 9/       | 69.5               | 66.5     | 66.5     | 66.5     | ė                  | 9        | 9                  |                    | 66.5     | 61.5               |                    |          | •                  |                    |
| Result     | No.         | 1                  | 7                  | m                  | 4                  | Ľ                  | 9                  | 7        | 80       | 6        | 10       | 11       | 12                 | 13       | 14       | 15       | 16                 | 17       | 18                 | 19                 | 20       | 21                 | 22                 | 23       | 24                 | 25                 |

| Aaw33805 Human H-t Aaw33805 Human alp Aay9729 Human alp Aay9729 Human alp Ada26627 Bacterial Abu36827 Bacterial Abu36829 Protein e Abu36829 Protein e Abu36829 Protein e Abu36839 Protein e Abu3781 Protein e Aaw53102 Pig H tra Aaw53102 Pig H tra Aaw90356 Swine alp Aaw97356 Swine alp Aay79302 Pig alpha Aay79302 Pig alpha Adx78379 Swine alp Adx83379 Caenorhab Adx83309 Bacterial Abb21896 Herbicida Abb21896 Herbicida                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |          |
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| AAR90572 AAW23805 AAW23805 AAW13805 AAV37279 AAC29230 AAC29230 AAC392823 ABU36823 ABU369163 AAW63102 AAW63102 AAW97356 AAW79302 AAW793095 AAW7930995                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |          |
| 00000000000000000000000000000000000000                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | )        |
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| 1188.99<br>1188.99<br>1198.99<br>1177.99<br>1177.99<br>1177.99                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |          |
| 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | 3        |
| 00000000000000000000000000000000000000                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | <u>,</u> |

## ALIGNMENTS

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This represents the N-terminal sequence of CHO O-fucosyltransferase. The enzyme can glycosylate an epidermal growth factor (EGF) domain of a polypeptide with an activated O-fucose residue. Inhibitors of O-fucosyltransferase, e.g. mutants with increased affinity for the EFG
 Human O-fucosyl:transferase able to glycosylate epidermal growth factor domains - useful for diagnosis and treatment of diseases involving overexpression of the enzyme.
 O-fucosyltransferase; epidermal growth factor; EGF; glycosylation; O-fucose; inhibitor; sensory neuron; retinal neuron; human.
 N-terminal amino acid sequence of CHO O-fucosyltransferase.
 Location/Qualifiers
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 /note= "unknown"
 Claim 5; Page 69; 90pp; English.
 AAW80572 standard; peptide; 61
 97US-00792498.
97US-00978741.
 97WO-US023401.
 (first entry)
 /note=
 (GETH) GENENTECH INC.
 Spellman MW;
 WPI; 1998-437477/37.
 Misc-difference 17
 Misc-difference
 Misc-difference
 Homo sapiens.
 17-DEC-1997;
 31-JAN-1997;
 26-NOV-1997;
 WO9833924-A1
 16-DEC-1998
 06-AUG-1998
 AAW80572;
 Wang Y,
RESULT 1
AAW80572
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Gaps

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Indels

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Mismatches

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54; Conservative

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Matches
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 This represents a the N-terminal sequence of the human heart O-fucosyltransferase that can glycosylate an epidermal growth factor (EGF) domain of a polypeptide with an activated O-fucose residue. Inhibitors of O-fucosyltransferase, e.g. mutants with increased affinity for the EFG domains, are used in diagnosis and treatment of conditions associated with overexpression of O-fucosyltransferase, to promote survival of sensory (retinal) neurons. Probes based on EGF domain polypeptide are used to detect gene amplification and expression. The expression can also be determined at the protein level using antibodies specific for O-fucosyltransferase
 ö
domains, are used in diagnosis and treatment of conditions associated with overexpression of O-fucosyltransferase, to promote survival of sensory (retinal) neurons. Probes based on EGF domain polypeptide are used to detect gene amplification and expression. The expression can also be determined at the protein level using antibodies specific for O-
 9
 1 RLAGSWDLAGYLLYXPXMGRFGNQADHFLGSLAFAKLXVRTLAVPPWIEYQHHKPPFTNL 60
 Human O-fucosyl:transferase able to glycosylate epidermal growth factor domains - useful for diagnosis and treatment of diseases involving
 1 RLAGSWDLAGYLLYXPXMGRFGNQADHFLGSLAFAKLXVRTLAVPPWIEYQHHKPPFTNL
 Gaps
 N-terminal amino acid sequence of human heart O-fucosyltransferase.
 O-fucosyltransferase, epidermal growth factor, EGF; glycosylation, O-fucose, inhibitor, sensory neuron; retinal neuron; human; heart.
 ;
0
 Length 61;
 Length 61;
 0; Indels
 98.2%; Score 320; DB 2; I
100.0%; Pred. No. 9.3e-38;
ive 0; Mismatches 0;
 Score 295; DB 2;
Pred. No. 3.5e-34;
 AAW80574 standard; peptide; 61 AA
 Claim 4; Page 69; 90pp; English.
 overexpression of the enzyme.
 97US-00792498.
97US-00978741.
 90.5%;
 97WO-US023401
 (first entry)
 61; Conservative
 (GETH) GENENTECH INC.
 Spellman MW;
 WPI; 1998-437477/37.
 Query Match
Best Local Similarity
 Query Match
Best Local Similarity
 fucosyltransferase
 Sequence 61 AA;
 Sequence 61 AA;
 61 H 61
 61 H 61
 16-DEC-1998
 WO9833924-A1.
 17-DEC-1997;
 31-JAN-1997;
26-NOV-1997;
 Homo sapiens
 06-AUG-1998
 AAW80574;
 Wang Y,
 RESULT
AAW8057
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 This represents a human heart O-fucosyltransferase that can glycosylate an epidermal growth factor (EGF) domain of a polypeptide with an activated O-fucose residue. Inhibitors of O-fucosyltransferase, e.g. dutants with increased affinity for the EFG domains, are used in diagnosis and treatment of conditions associated with overexpression of fucosyltransferase, to promote survival of sensory (retinal) neurons. Probes based on EGF domain polypeptide are used to detect gene amplification and expression. The expression can also be determined at the protein level using antibodies specific for O-fucosyltransferase
 61
 61
 61
 3 AGSWDPAGYLLYCPCMGRFGNQADHFLGSLAFAKLLNRTLAVPPWIEYQHHKPPFTNLH 61
 Human O-fucosyl:transferase able to glycosylate epidermal growth factor domains - useful for diagnosis and treatment of diseases involving
 3 AGSWDPAGYLLYCPCMGRFGNQADHFLGSLAFAKLLNRTLAVPPWIEYQHHKPPFTNLH
 3 AGSWDLAGYLLYXPXMGRFGNQADHFLGSLAFAKLXVRTLAVPPWIEYQHHKPPFTNLH
3 AGSWDLAGYLLYXPXMGRFGNQADHFLGSLAFAKLXVRTLAVPPWIEYQHHKPPFTNLH
 Gaps

 .61
 /note= "N-terminal sequence claimed for in claim 4"

 O-fucosyltransferase; epidermal growth factor; EGF; glycosylation; O-fucose; inhibitor; sensory neuron; retinal neuron; human; heart.
 .
0
 ch 90.5%; Score 295; DB 2; Length 365;
1 Similarity 91.5%; Pred. No. 2.9e-33;
54; Conservative 0; Mismatches 5; Indels
 Location/Qualifiers
 ABM82223 standard; protein; 388 AA.
 AAW80571 standard; protein; 365 AA
 Example 1; Fig 12A; 90pp; English.
 Human heart O-fucosyltransferase.
 domains - useful for diagnosi
overexpression of the enzyme.
 97US-00792498.
97US-00978741.
 97WO-US023401
 (first entry)
 (GETH) GENENTECH INC.
 Wang Y, Spellman MW;
 1998-437477/37.
 Query Match
Best Local Similarity
 N-PSDB; AAV65632
 Sequence 365 AA;
 31-JAN-1997;
26-NOV-1997;
 Homo sapiens
 WO9833924-A1
 17-DEC-1997;
 16-DEC-1998
 06-AUG-1998.
 Peptide
 Best Loc
Matches
 RESULT 3
 RESULT 4
ABM82223
ID ABM8
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Human O-fucosyltransferase sequence expressed by a plasmid insertion.

(first entry)

16-DEC-1998

AAW80573;

O-fucosyltransferase; epidermal growth factor; EGF; glycosylation; O-fucose; inhibitor; sensory neuron; retinal neuron; human; heart.

Homo sapiens. Synthetic.

27. .32 /note≃ "polyhistidine tag" Location/Qualifiers

97WO-US023401. 97US-00792498 97US-00978741

17-DEC-1997; 31-JAN-1997;

06-AUG-1998.

WO9833924-A1

Peptide

(GETH ) GENENTECH INC.

26-NOV-1997;

Spellman MW;

Wang Y,

WPI; 1998-437477/37.

N-PSDB; AAV65633

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The invention relates to human tumour-associated antigenic target (TAT) polypeptides, and their related nucleic acids. The TAT polypeptides are overexpressed in cancer tissues compared to normal tissues, and may thus serve as effective targets for the diagnosis and treatment of cancer in mammals. The invention also relates to nucleic acid and polypeptide sequences at least 80% identical to the TAT nucleic acids and polypeptides; expression vectors and host cells comprising a TAT nucleic acid; an antibody specific for a TAT polypeptide; a peptide or organic molecule which binds to a TAT polypeptide; fusion proteins comprising a TAT polypeptide; and methods and compositions for the treatment or TAT polypeptides, nucleic acids, antibodies, antagonists, binding molecules and compositions are useful for diagnosing or treating a cell proliferative disorder associated with increased TAT expression, particularly cancers such as breast cancer, colorectal cancer, lung cancer, cancer, liver cancer, bladder cancer, pancreatic cancer, cervical cancer, cancers of the central cancer, services system melanoma and leukaemia. TAT nucleic acids may further be cancer as which is a but the cancer and leukaemia.
 Tumour-associated antigenic target (TAT) polypeptide PRO83146, SEQ:5726.
 New tumor-associated antigenic target polypeptides and nucleic acids, useful in preparing a medicament for treating or detecting a proliferative disorder, e.g. breast, lung, colorectal, ovarian or
 used as hybridisation probes, in chromosome and gene mapping, in chromosome identification and in gene therapy. The present sequence represents a TAT polypeptide of the invention
 Tumour-associated antigenic target; TAT; human; overexpression; ctumour; diagnosis; cell proliferative disorder; breast cancer; colorectal cancer; lung cancer; ovarian cancer; liver cancer; central nervous system cancer; blader cancer; pancreatic cancer; cervical cancer; melanoma; leukaemia; hybridisation probe; chromosome identification; chromosome mapping; gene mapping;
 Length 388;
 Match 90.5%; Score 295; DB 8; Length 38 Local Similarity 91.5%; Pred. No. 3.1e-33; les 54; Conservative 0; Mismatches 5; Indels
 Claim 12; SEQ ID NO 5726; 7273pp; English
 29-SEP-2003; 2003WO-US028547.
 02-OCT-2002; 2002US-0414971P
 (first entry)
 prostate cancer or tumor.
 gene therapy; cytostatic
 (GETH) GENENTECH INC
 WPI; 2004-347921/32.
 Zhang Z,
 N-PSDB; ACN40746.
 Sequence 388 AA;
 WO2004030615-A2
 Homo sapiens.
 18-NOV-2004
 15-APR-2004
ABM82223;
 Query Match
 Wu TD,
```

Human O-fucosyl:transferase able to glycosylate epidermal growth factor domains - useful for diagnosis and treatment of diseases involving

Example; Fig 13B; 90pp; English.

overexpression of the enzyme.

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ö
 This represents the amino acid sequence of the human heart Offucosyltransferase expressed by a plasmid insertion. The human Offucosyltransferase can glycosylate an epidermal growth factor (EGF) domain of a polypeptide with an activated Offucose residue. Inhibitors of Offucosyltransferase, e.g. mutents with increased affinity for the EFG domains, are used in diagnosis and treatment of conditions associated with overexpression of Offucosyltransferase, to promote survival of sensory (retinal) neurons. Probes based on EGF domain polypeptide are used to detect gene amplification and expression. The expression can also be determined at the protein level using antibodies specific for O
 Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 61
 35 AGSWDPAGYLLYCPCMGRFGNQADHFLGSLAFAKLINRTLAVPPWIEYQHHKPPFTNLH 93
 3 AGSWDLAGYLLYXPXMGRFGNQADHFLGSLAFAKLXVRTLAVPPWIEYQHHKPPFTNLH
 Gaps
 ö
 Length 397;
 Indels
 Score 295; DB 2; Ler
Pred. No. 3.2e-33;
 Ä.
 AAM78377 standard; protein; 417
 ô
 Human protein SEQ ID NO 1039.
 90.5%;
 (first entry)
 Local Similarity 91.5
les 54; Conservative
 fucosyltransferase
 Sequence 397 AA;
 06-NOV-2001
 AAM78377;
 Query Match
 Matches
 RESULT 6
AAM78377
MX BX BX BX BX B
 셤
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ö

Gaps

; 0

84 61

3 AGSWDLAGYLLYXPXMGRFGNQADHFLGSLAFAKLXVRTLAVPPWIEYQHHKPPFTNLH AGSWDPAGYLLYCPCMGRFGNQADHFLGSLAFAKLINRTLAVPPWIEYQHHKPPFTNLH

Best Loc Matches

δ

AAW80573 standard; protein; 397 AA

RESULT 5
AAW80573
ID AAW8

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nervous system disorder; arthritis; inflammation.
 (HYSE-) HYSEQ INC.
 Sequence 417 AA;
 N-PSDB; AAK52494
 WO200157190-A2
 16-DEC-1998
 Homo sapiens
 AAW80577;
 Matches
 RESULT 8
AAW80577
 ò
 g
 The invention relates to polynucleotides (AAX51456-AAX53435) and the encoded polypeptides (AAX7823-AAM80302) that exhibit activity elating to eytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissus growth factor activity, immunomodulatory activity and activity, tissus growth factor activity, immunomodulatory activity and activity indunadulating and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 211 (AAK52582) and 3666 (AAM80203) are omitted as the relevant pages from the sequence listing were missing at the time of publication
 1;
 Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy.
 Human, cytokine, cell proliferation, cell differentiation, gene therapy, vaccine, peptide therapy, stem cell growth factor, haematopoiesis, tissue growth factor, immunomodulatory, cancer, leukaemia,
 7 DLAGYLLYXPXM-----GRFGNQADHFLGSLAFAKLXVRTLAVPPWIEYQHHKPPFTNLH 61
 Xu C, Cao Y;
, Chen R, Wang ZW;
 5; Gaps
vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
 / Match 71.3%; Score 232.5; DB 4; Length 417; Local Similarity 73.3%; Pred. No. 3e-24; Indels 5; res 44; Conservative 4; Mismatches 7; Indels 5;
 Drmanac RT, Asundi V, Zhou P, Ku
Wang D, Wang J, Zhang J, Ren F,
Wejhrman T, Goodrich R;
 Claim 20; Page 3276-3277; 6221pp; English.
 AAM79361 standard; protein; 417 AA
 03-FEB-2000; 2000US-00496914.
27-AFR-2000; 2000US-00560B75.
20-UDN-2000; 2000US-0059075.
19-UJL-2000; 2000US-0063225.
01-SEP-2000; 2000US-00654936.
15-SEP-2000; 2000US-0063361.
20-CT-2000; 2000US-0063325.
30-NOV-2000; 2000US-00728422.
 Tang YT, Liu C, Drmanac RT,
Ma Y, Zhao QA, Wang D, Wang
Xue AJ, Yang Y, Wejhrman T,
 Human protein SEQ ID NO 3007.
 05-FEB-2001; 2001WO-US004098
 (first entry)
 WPI; 2001-476283/51.
 (HYSE-) HYSEQ INC.
 N-PSDB; AAK51510
 Sequence 417 AA;
 WO200157190-A2
 Homo sapiens.
 06-NOV-2001
 09-AUG-2001.
 Query Match
Best Local S:
Matches 44
 AAM79361;
 RESULT 7
 AAM79361
 ઠે
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The invention relates to polynuclectides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM89302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides are useful in gene therapy, vaccines or e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity tissue growth factor activity, immunomodulatory activity and activity tissue growth factor activity, immunomodulatory activity and inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111 inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111 sequence listing were missing at the time of publication
 Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy.
 ZW;
 Partial human sequence of unknown function from a myeblast cell line.
 5; Gaps
 Xu C, Cao Y;
, Chen R, Wang
 O-fucosyltransferase; epidermal growth factor; EGF; glycosylation; O-fucose; inhibitor; sensory neuron; retinal neuron; human; heart.
 67.6%; Score 220.5; DB 4; Length 417; 70.0%; Pred. No. 1.5e-22; ive 5; Mismatches 8; Indels 5;
 Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xv
Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F,
Xue AJ, Yang Y, Wejhrman T, Goodrich R;
 Claim 20; Page 229-230; 6221pp; English.
 AAW80577 standard; protein; 343 AA.
 03-FEB-2000; 2000US-00496914.
27-APR-2000; 2000US-00560875.
20-UTW-2000; 2000US-00590075.
19-UTW-2000; 2000US-00620325.
01-SEP-2000; 2000US-00654936.
15-SEP-2000; 2000US-0063561.
20-CTT-2000; 2000US-0063325.
05-FEB-2001; 2001WO-US004098
 (first entry)
 42; Conservative
 Query Match
Best Local Similarity
 2001-476283/51.
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61

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Human O-fucosyl:transferase able to glycosylate epidermal growth factor domains - useful for diagnosis and treatment of diseases involving overexpression of the enzyme.
 The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of
 New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
 insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL10511), expressed DNA sequences (ABL16176) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 O-fucosyltransferase; epidermal growth factor; EGF; glycosylation; O-fucose; inhibitor; sensory neuron; retinal neuron; human; heart.
 Disclosure; SEQ ID NO 18162; 21pp + Sequence Listing; English
 N-terminal sequence of expressed human O-fucosyltransferase.
 Score 177; DB 4; Length 402;
Pred. No. 2.5e-16;
3; Mismatches 9; Indels
 7 DLAGYLLYXPXMGRFGNQADHFLGSLAFAKLXVRTLAVPPWIEYQ 51
 DPNGYLTYCPCMGRFGNQADHFLGSLAFAKALNRTLILPPWVEYR 72
 54.3%; Scor. 73.3%; Pred. No. z...
 Location/Qualifiers
 ¥.
 Example 1; Page 39; 90pp; English.
 /note= "unknown"
 /note= "unknown"
 AAW80575 standard; protein; 28
 97WO-US023401
 97US-00792498
 97US-00978741
 16-DEC-1998 (first entry)
 33; Conservative
 (GETH) GENENTECH INC.
 Spellman MW;
 WPI; 1998-437477/37.
WPI; 2001-656860/75.
N-PSDB; ABL07893.
 Local Similarity
 Misc-difference 23
 Sequence 402 AA;
 Misc-difference
 interactions.
 17-DEC-1997;
 Homo sapiens
Synthetic.
 WO9833924-A1
 31-JAN-1997;
 26-NOV-1997;
 06-AUG-1998
 AAW80575;
 Query Match
 Wang Y,
 Matches
 RESULT 10
 AAW805
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 This represents a published partial human sequence of unknown function from a myeblast cell line. The invention provides a human heart O-fucosyltransferase enzyme that can glycosylate an epidermal growth factor (EGF) domain of a polypeptide with an activated O-fucose residue. Inhibitors of O-fucosyltransferase, e.g. mutants with increased affinity associated with overexpression of O-fucosyltransferase, to promote survival of sensory (retinal) neurons. Probes based on EGF domain expression contact and expression and expression. The expression can also be determined at the protein level using antibodies specific for O-fucosyltransferase
 Human O-fucosyl:transferase able to glycosylate epidermal growth factor domains - useful for diagnosis and treatment of diseases involving overexpression of the enzyme.
 Gaps
 Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.
 ..
0
 Length 343;
 Indels
 Drosophila melanogaster polypeptide SEQ ID NO 18162.
 61
 1 NOADHFLGSLAFAKLLNRTLAVPPWIEYOHHKPPFTNLH 39
 62.6%; Score 204; DB 2; Lk
94.9%; Pred. No. 2.8e-20;
iive 0; Mismatches 2;
 23 NQADHFLGSLAFAKLXVRTLAVPPWIEYQHHKPPFTNLH
 Myers EW;
 Example 1; Page 62-68; 90pp; English.
 ABB63790 standard; protein; 402 AA
 Li PWD,
 97US-00792498.
97US-00978741.
 23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150
 97WO-US023401.
 23-MAR-2001; 2001WO-US009231
 (first entry)
 Best Local Similarity 94.9
Matches 37; Conservative
 Drosophila melanogaster
 (GETH) GENENTECH INC
 Wang Y, Spellman MW;
 Adams M,
 WPI; 1998-437477/37.
 CORP NY
 N-PSDB; AAV65634.
 Sequence 343 AA;
 WO200171042-A2
 WO9833924-A1
 17-DEC-1997;
 31-JAN-1997;
 26-NOV-1997;
 26-MAR-2002
 Venter JC,
 27-SEP-2001
 06-AUG-1998
 (PEKE) PE
 Query Match
 RESULT 9
 ABB63790
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Gaps

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invention

us-09-774-954-3.rag

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 This represents the N-terminal amino acid sequence of the human heart O-fucosyltransferase expressed by a plasmid insertion. The human O-fucosyltransferase can glycosylate an epidermal growth factor (EGF) domain of a polypeptide with an activated O-fucose residue. Inhibitors of O-fucosyltransferase, e.g. mutants with increased affinity for the EFG domains, are used in diagnosis and treatment of conditions associated with overexpression of O-fucosyltransferase, to promote survival of sensory (tetinal) neurons. Probes based on EGF domain polypeptide are used to detect gene amplification and expression. The expression can also be determined at the protein level using antibodies specific for O-fucosyltransferases.
 Human, signal peptide-containing protein, HSPP; diagnosis; cancer; inflammation; cardiovascular disease; anticancer; anti-inflammatory; antimicrobial; nootropic; neuroprotective; cardiovascular; hepatotropic; antiasthmatic; gene therapy; cell proliferation; neurological disorder; reproductive disorder; developmental disorder; arteriosclerosis; cirrhosis psoriasis; acquired immune deficiency syndrome; anaemia; asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia; Parkinson's disease; Huntington's disease; ovulatory defect;
 New human signal peptide-containing proteins useful in treatment, prevention and diagnosis of e.g. cancer, inflammation and cardiovascular
 YT, Gorgone GA, Corley NC, Guegler KJ, Baughn MR;
Au-Young J, Yue H, Patterson C, Reddy R, Hillman JL;
 Gaps
 .
0
 Human signal peptide containing protein HSPP-102 SEQ ID NO:102.
 24.8%; Score 81; DB 2; Length 28; 94.4%; Pred. No. 0.00057; tive 0; Mismatches 1; Indels
 Claim 1; Page 225-226; 327pp; English.
 AAY87325 standard; protein; 150 AA.
 3 AGSWDLAGYLLYXPXMGR 20
 28
 98US-0090762P.
98US-0094983P.
98US-0102686P.
98US-0112129P.
 99WO-US014484.
 11 AGSWDPAGYLLYXPXMGR
 11-MAY-2000 (first entry)
 Local Similarity 94.4 les 17; Conservative
 PHARM INC.
 WPI; 2000-160673/14.
N-PSDB; AAZ98210.
 Eucosyltransferase
 muscular dystrophy
 Sequence 28 AA;
 (INCY-) INCYTE
 WO200000610-A2.
 Lal P, Tang Y
Akerblom IE,
Bandman O;
 31-JUL-1998;
01-OCT-1998;
11-DEC-1998;
 25-JUN-1999;
 Homo sapiens
 26-JUN-1998;
 06-JAN-2000
 AAY87325;
 Query Match
Best Local S
 disease.
 Matches
 RESULT 11
¥8888888888888888
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AAZ98109 to AAZ98242 encode AAY87224 to AAY87357 which represent

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buman signal peptide-containing proteins HSPP-1 to HSPP-134. HSPPs have anticancer, anti-inflammatory, antimicrobial, nootropic, hepatotropic, cardiovascular and antiaschmatic activities, and can be used in gene therapy. HSPPs can be used to treat or prevent disorders associated with decreased activity or function of HSPP. Antagonists of associated with decreased activity or function of HSPP. Antagonists of activity or function of HSPP. Such diseases include cell proliferation (including cancer), inflammation, cardiovascular, neurological, reproductive or developmental disorders, (e.g. arteriosclerosis, cirrhosis, psoriasis, adquired immune deficiency syndrome, anaemis, cirrhosis, psoriasis, adquired immune deficiency syndrome, anaemis, circhast, psoriasis, additional or other infections, congestive or ischaemic heart disease, Alzheiner's Parkinson's or Huntingcon's congestive or detecting HSPP in standard hybridisation and maplification assays (for detecting HSPP in standard hybridisation and maplification assays (for diagnosis and monitoring), in gene therapy, as antisense, triplex-forming variations, and for chromosomal mapping HSPP are also used to raise (specific antibodies (Ab) and to screen for adounces or genetic specific antibodies (Ab) and to screen for adounces or genetic specific antibodies (Ab) and to screen for adounces or genetic specific antibodies (Ab) and to screen for adounces or genetic concentic agents). As therapeutic antagonists in competitive drug screens, and for purification of HSPP from natural immunoassays), as therapeuticanted or adounces in an expension of HSPP in natural immunoassays).
 ö
 screening
 Antisense; prokaryotic essential gene; cell proliferation; drug design.
 Zyskind JW;
Xu HH;
 Gaps
 New antisense nucleic acids, useful for identifying proteins or scre
for homologous nucleic acids required for cellular proliferation to
isolate candidate molecules for rational drug discovery programs.
 ;
 Score 76; DB 3; Length 150;
Pred. No. 0.022;
 3; Indels
 Ohlsen KL,
Forsyth RA,
 Protein encoded by Prokaryotic essential gene #19393.
 Haselbeck R,
Yamamoto R,
 1; Mismatches
 ABU33866 standard; protein; 198
 Malone C,
Carr GJ,
 26 AGSWDPAGYLLYCPCMGK 43
 3 AGSWDLAGYLLYXPXMGR 20
 21-MAR-2001, 2001US-00815242.
06-SEP-2001, 2001US-00948993.
25-0CT-2001, 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002, 2002US-0362699P.
 21-MAR-2002; 2002WO-US009107.
 23.3%;
 (first entry)
 Query Match
Best Local Similarity 77.8
Matches 14; Conservative
 (ELIT-) ELITRA PHARM INC.
 Zamudio C,
Trawick JD,
 Mycobacterium avium.
 WPI; 2003-029926/02.
 N-PSDB; ACA37736.
 Sequence 150 AA;
 WO200277183-A2.
 19-JUN-2003
 03-OCT-2002.
 ABU33866;
 Wang L,
Wall D,
 RESULT 12
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 The invention relates to an isolate and acts compitating any one to the nucleic acid inhibits proliferation of a cell. Also included are:

Co the nucleic acid inhibits proliferation of a cell. Also included are:

Co of the nucleic acid inhibits proliferation of a cell. Also included are:

Co concoding a polypeptide whose expression is inhibited by the antisense contisense nucleic acid, (4) an antibody capable of specifically brinding catisses nucleic acid, (4) an antibody capable of specifically brinding the polypeptide, (5) producing the polypeptide, (6) inhibited by the activity of a gene in an operon required for proliferation or the activity of a gene in an operon required for proliferation, (7) identifying a compound that influences the activity of required for proliferation, or that has an activity against a biological pathway or the gene product or that has an activity against a biological pathway or required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation of an organism acts; (9) manufacturing an antibictic; (10) profiling a compound that inhibits proliferation of an organism acts; (9) manufacturing an antibictic; (10) profiling the extent or organism acts; (1) identifying the target of a compound that inhibits the gene product is overexpressed or undersexpressed; (12) determining the extent or which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for each all an earth and an organism or screening for homologous nucleic acids required for artional and all an earth and a proportions or screening for possible models are useful for an an each and a proportion or the search of the strains and the strains and the proportion and an organism. The antisense nucleic acids are useful for an an analyse or screening for homologous nucleic acids are useful for an an antisense mucleic acids are u
 ä
 drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
 The invention relates to an isolated nucleic acid comprising any one of
 Gaps
 Opperman T, Houseweart CE;
 Antibacterial; Gene therapy; Vaccine; Streptococcus pneumoniae.
 ä
 21.3%; Score 69.5; DB 6; Length 198; 50.0%; Pred. No. 0.25; ive 2; Mismatches 11; Indels
 Streptococcus pneumoniae protein, Seq ID No 5075.
 FGRÓVDSFEGDIAFAGLDVPVRAVFIRAPWVE 147
 21 FGNQADHFLGSLAFAKLXVRTLAV---PPWIE 49
Claim 25; SEQ ID NO 61790; 1766pp; English.
 ftp.wipo.int/pub/published_pct_sequences
 Zeng Q,
 ADK48560 standard; protein; 737 AA
 THERAPEUTICS CORP
 97US-0051553P.
98US-0085131P.
98US-00107433.
 26-MAY-2000; 2000US-00583110
 Bush D,
 20-MAY-2004 (first entry)
 Local Similarity 50.0
les 16; Conservative
 Streptococcus pneumoniae
 Doucette-Stamm L,
 Sequence 198 AA;
 (GENO-) GENOME
 02-JUL-1997;
 US6699703-B1
 12-MAY-1998;
 02-MAR-2004
 116
 Query Match
 Best Loc
Matches
 RESULT 13
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1;
 New proteins and nucleic acid molecules from Streptococcus pneumoniae, useful as medicaments for treating or preventing a disease or infection due to streptococcus bacteria, such as pneumonia, sepsis, otitis media or
 The invention relates to isolated Streptococcus pneumoniae nucleic acids and polypeptides. The nucleic acids and proteins are useful for indiagnosing, preventing and treating pathological conditions resulting from bacterial infection, such as S. pneumoniae infection. These may also be used for drug screening procedures. The present sequence represents a Streptococcus pneumoniae polypeptide of the invention. Note: The sequence data for this patent did not appear in the printed specification but was obtained in electronic format directly from USPTO at
 Bacterial meningitis; pneumonia; sepsis; otitis media; ear infection; antiinflammatory; antibacterial; immunostimulant; auditory; respiratory; gene therapy; vaccine.
 New nucleic acid molecules and polypeptides useful for diagnosing, preventing and treating pathological conditions resulting from bacterial infection, e.g. Streptococcus pneumoniae infection, and in drug
 The invention relates to a protein comprising or having at least 50% identity to any of the 2469 amino acid sequences, identified in the
 Gaps
 3;
 Length 737;

 s. pneumoniae type 4 strain protein from coding region #849.

 Indels
 8 LAGYLLYXPXMGRFGNQADHFLGSLAFAKLXVRTLAVPPWIEY
 ..
8
 DB
 20.4%; Scur.
37.2%; Pred. No. 5...
 Disclosure; SEQ ID NO 5075; 301pp; English
 Streptococcus pneumoniae; type 4 strain.
 Claim 1; SEQ ID NO 1698; 56pp; English.
 Masignani V, Tettelin H, Fraser C;
 ABU01274 standard; protein; 741 AA
 seqdata.uspto.gov/sequence.html
 27-MAR-2002; 2002WO-IB002163.
 27-MAR-2001; 2001GB-00007658
 (first entry)
 16; Conservative
 (CHIR-) CHIRON SPA.
(GENO-) INST GENOMIC RES
 (revised)
 WPI; 2003-040579/03
 Best Local Similarity
 N-PSDB; ABX06561
WPI; 2004-212399,
N-PSDB; ADK45899
 Sequence 737 AA;
 WO200277021-A2.
 23-OCT-2003
11-FEB-2003
 3-OCT-2002
 ABU01274;
 screening
 Query Match
 Matches
 ABU0127
 RESULT
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expressed from 2469 of 2489 identified DNA coding regions from the expressed from 2469 of 2489 identified DNA coding regions from the Streptococcus pneumoniae type 4 strain genomic sequence appearing as treating a patient by administering the protein, DNA or antibody (in a composition), a kit comprising first and second primers, which are the nucleic acid cited above or fragments between nucleotides 8-100 of a sequence contained within a Streptococcus nucleic acid sequence, where the first primer is substantially complementary to the target sequence and the second primer is substantially complementary to the target sequence to the target sequence, and where the parts of the primers having substantially complementary to the complement of the target sequence or and the second primer is substantially complementary to the complement of be amplified, assay comprising contacting a test compound with the protein, and determining whether the test compound binds to the protein and a Streptococcus pneumoniae bacterium, where one or more genes conding the proteins has been rendered inactive. The proteins, nucleic acid molecules, antibody and compositions are useful as medicaments for treating or preventing a disease or infection due to streptococcus cand antibodics. The methods are useful for identifying immunodominant proteins. The present sequence is one of the 4469 proteins capted and antibodics. The methods are useful for identified composition of the printed sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the printed specification, but was obtained in electronic format directly from WIPO at the property of the printed specification, but was obtained in electronic format directly from WIPO at the property of the printed specification, but was obtained in electronic format directly from WIPO at the property of the printed specification, but was obtained in electronic format directly from WIPO at the property of the property of the
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 3; Gaps
 New isolated nucleic acid encoding a Streptococcus pneumoniae polypeptide, useful for diagnosing, preventing and/or treating
 20.4%; Score 66.5; DB 6; Length 741; 37.2%; Pred. No. 3.2; ative 5; Mismatches 19; Indels 3
 Meningitis; bacteraemia; pneumonia; otitis media; vaccine; bacterial infection.
 114 LIGVALYIPTAFLFSNIGTYFIGSIL---ILVGSLLVSPWSVY 153
 8 LAGYLLYXPXMGRFGNQADHFLGSLAFAKLXVRTLAVPPWIEY 50
 Novel S. pneumoniae protein sequence, SEQ ID 3610.
 ADR94975 standard; protein; 763 AA.
 (GENO-) GENOME THERAPEUTICS CORP.
 98US-00107433.
 97US-0051553P.
98US-0085131P.
 Doucette-Stamm LA, Bush D;
 16-DEC-2004 (first entry)
 Query Match
Best Local Similarity 37.29
 Streptococcus pneumoniae.
 WPI; 2004-697205/68.
N-PSDB; ADR92372.
 Seguence 741 AA;
 JS6800744-B1.
 30-JUN-1998;
 02-JUL-1997;
12-MAY-1998;
 05-OCT-2004.
 ADR94975;
 THE STANDARD
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The invention relates to an isolated nucleic acid comprising a sequence encoding a Streptococcus pneumoniae ADR91366polypeptide, or its fragments, with any of 9 fully defined sequences (appearing as ADR94308, ADR94699, ADR94690, ADR94690, ADR94690, ADR94600, ADR94600, ADR94600, ADR94600, ADR94600, ADR94600, ADR94600, ADR95600, ADR956000 or any of the fully defined sequences appearing as ADR941005, ADR950079) and ADR95197, ADR95234, ADR93039, ADR950079, ADR95186, ADR95186, ADR93187, ADR93187, ADR93039, ADR93039, ADR93186, ADR93187005, ADR93186, ADR9318700 or and consecutive nuclectides of the nucleotide sequences. Or an under high stringency conditions to the nucleotide sequences. The nucleic acids and proteins are chosen from 5206 disclosed sequences. The nucleic acids and proteins are chosen from 5206 disclosed sequences. The nucleic acids and proteins are comprising the recombinant expression vector and a probe comprising at least 20 consecutive nucleotides of the nucleotide comprising at least 20 consecutive nucleotides of the nucleotide comprising at least 20 consecutive nucleotides of the nucleotide comprising at least 20 consecutive nucleotides of the nucleotide comprising at least 20 consecutive nucleotides of the nucleotide of invention are useful for the diagnosis, prevention and/or treatment of streptococcus pneumoniae e.g. pneumoniae acompositions of the present sequences and approach of the present sequences. Note: The sequence data for this patent did content of the printed specification, but was obtained in directly from USPPO at the present beautified the printed specification, but was obtained in the present beautified the printed specification of the 2003 disclosed sequences and and processed to the present beautified the printed specification, but was obtained in the printed processed to the present beautified the printed specification of the 2003 disclosed sequences and approach processed to the present beautified the present beautified to the present beautified to the present beautified to t
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 3; Gaps
pathological conditions resulting from the bacterial infection.
 Query Match
20.4%; Score 66.5; DB 8; Length 763;
Best Local Similarity 37.2%; Pred. No. 3.4;
Matches 16; Conservative 5; Mismatches 19; Indels 3
 166 LIGVALYIPTAFLFSNIGTYFIGSIL---ILVGSLLVSPWSVY 205
 8 LAGYLLYXPXMGRFGNOADHFLGSLAFAKLXVRTLAVPPWIEY 50
 electronic format directly from USPTO at segdata.uspto.gov/sequence.html?DocID=6800744B1
 Disclosure, SEQ ID NO 3610; 151pp; English.
 Sequence 763 AA;
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Search completed: October 25, 2005, 15:30:40 Job time : 41.8296 secs

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Query Match
Best Local Similarity
Matches 61; Conserv
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 October 25, 2005, 15:25:36; Search time 10.0205 Seconds (without alignments) 454.426 Million cell updates/sec
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Sequence 6, Ap
Sequence 17, Ap
Sequence 11, A
Sequence 13, A
Sequence 8, Ap
Sequence 12, A
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Sequence 11, A
Sequence 11, A
Sequence 11, A
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Sequence 9,
 Description
 Sequence 3
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Sequence
Sequence
Sequence
 Sequence
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Sequence
 Sequence
 Sequence
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 GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-08-978-741.14
US-09-333-729A-14
US-09-583-110-5075
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US-08-978-741-6
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US-08-333-729A-13
 PCT-US91-00899-11
US-07-914-281-6
 Total number of hits satisfying chosen parameters:
 US-09-333-729A-4
 513545 seqs, 74649064 residues
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 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 - protein search, using sw model
 BLOSUM62
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 Minimum DB seq length: 0
Maximum DB seq length: 200000000
 US-09-774-954-3
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Match Length
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Perfect score:
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 Sequence 3
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 98.2%; Score 320; DB 3; Length 61; 100.0%; Pred. No. 1e-35;
US-09-042-531-6
US-09-254-077A-11
US-09-294-016-11353
US-09-18-111-5
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US-09-568-472-5
 ZIP: 94060
COMPUTER READABLE FORM:
MEDIUW TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IEBM PC compatible COMPUTER: IEBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Winheatin (Genentech) CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,741
FILING DATE: 26-No. 6100076-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/792498
FILING DATE: 31
ATTORNEY/AGENT INFORMATION:
NAME: SVODOGA: CTAIG 9
REFERENCE/DOCKET NUMBER: 39,044
REFERENCE/DOCKET NUMBER: 39,044
REFERENCE/DOCKET NUMBER: 39,044
TELEPHONE: 650/252-9881
TELEPHONE: 650/252-9881
 Sequence 3, Application US/08978741
Patent No. 6100076
GENERAL INFORMATION:
TITLE OF INVENTION: O-Fucosyltransferase
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA WAY
 100.0%; Prec. ...
 ALIGNMENTS
 CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
 INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
 LENGTH: 61 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
 61; Conservative
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Query Match 90.5%; Score 295; DB 3; Length 61; Best Local Similarity 91.5%; Pred. No. 2.3e-32; Matches 54; Conservative 0; Mismatches 5; Indels
 Length 61;
 / Match 90.5%; Score 295; DB 3; Length 61 Local Similarity 91.5%; Pred. No. 2.3e-32; Local Similarity 91.5%; Pred. No. 2.3e-32; Indels nes 54; Conservative 0; Mismatches 5; Indels
 AUDRESSEE: Genentch, Inc.
STREET: 1 DNA WAY
CITY: South San Francisco
STRATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
WEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Win PC compatible
COMPUTER: WinPatin (Genentcch)
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 APPLICANT: Wang Yang
APPLICANT: Wang Yang
APPLICANT: Wang Yang
APPLICANT: Spellman, Michael W.
TITLE OF INVENTION: O-PUCOSyltransferase
FILE REFERENCE: P1041P1D1-Substitute
CURRENT APPLICATION NUMBER: US/09/333,729A
CURRENT FILING DATE: 1999-06-15
PRIOR APPLICATION NUMBER: US 08/798,741
PRIOR FILING DATE: 1997-11-26
SEQ ID NO 4 EQ ID NOS: 21
 RESULT 5
US-08-978-741-2
US-08-978-741-2
Sequence 2, Application US/08978741
Patent No. 6100076
GENERAL INFORMATION:
APPLICANT: Yang Wang, Michael W. Spellman;
TITLE OF INVENTION: O-Fucosyltransferase
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
 Sequence 4, Application US/09333729A; Patent No. 6270987
 TELBFAX: 650/952-9881
INPORMATION FOR EEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 61 amino acids
TYPE: Amino Acid
TOPOLOXY: Linear
 TYPE: PRT
ORGANISM: Homo Sapien
 GENERAL INFORMATION:
TELEPHONE:
 US-09-333-729A-4
 US-09-333-729A-4
 US-08-978-741-9
 LENGTH: 61
 Query Match
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 1 RLAGSWDLAGYLLYXPXMGRFGNQADHFLGSLAFAKLAVRTLAVPFWIEYQHHKPPFTNL 60
 1 RLAGSWDLAGYLLYXPXMGRFGNQADHFLGSLAFAKLXVRTLAVPPWIEYQHHKPPFTNL 60
 Query Match 98.2%; Score 320; DB 3; Length 61; Best Local Similarity 100.0%; Pred. No. 1e-35; Matches 61; Conservative 0; Mismatches 0; Indels
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 1BM PC compatible
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COMPUTER: 1BM PC compatible
COMPUTER: 15.000 MB PC COMPUTER: 10.000 MB PC MB PC COMPUTER: 10.000 MB PC MB
 Sequence 5, Application US/0933729A;
Sequence 5, Application US/0933729A;
Farent No. 6270987;
APPLICANT: Mang.Yang
APPLICANT: Mang.Yang
TITLE OF INVENTION: O.Fucosyltransferase;
FILE REFERENCE: P1041P1D-Substitute;
CURRENT PILION NUMBER: US/09/333,729A;
CURRENT FILING DATE: 1999-06-15;
PRIOR FILING DATE: 1999-06-15;
NUMBER OF SEQ ID NOS: 21
LENTH: 61
 Sequence 9, Application US/08978741
Patent No. G100076
GENERAL INFORMATION:
APPLICANT: Yang Wang, Michael W. Spellman
TITLE OF INVENTION: O-Pucosyltransferase
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
 FEATURE:
NAME/KEY: unsure
LOCATION: 15, 17, 38
CTHER INFORMATION: unknown amino acid
US-09-333-729A-5
 P1041P1
 NAME: Svoboda, Craig G. REGISTRATION NUMBER: 39,044 REFERENCE/DOCKET NUMBER: PIC TELECOMMUNICATION INFORMATION:
 ADDRESSEE: Genentech, Inc. STREET: 1 DNA Way CITY: South San Francisco STATE: California COUNTRY: USA
 TYPE: PRT
ORGANISM: Cricetulus Grieseus
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 61 H 61
 61 H 61
 RESULT 3
US-08-978-741-9
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3 AGSWDLAGYLLYXPXMGRFGNQADHFLGSLAFAKLXVRTLAVPPWIEYQHHKPPFTNLH 61
 3 AGSWDLAGYLLYXPXMGRFGNQADHFLGSLAFAKLXVRTLAVPPWIEYQHHKPPFTNLH 61
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 3 AGSWDPAGYLLYCPCMGRFGNQADHFLGSLAFAKLLNRTLAVPPWIEYQHHKPPFTNLH 61
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Pred. No. 1.8e-31;
0; Mismatches 5; Indels
 Length 365;
 Score 295; DB 3; Length 36
Pred. No. 1.8e-31;
0; Mismatches 5; Indels
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible
 APPLICANT: Wang, Yang
APPLICANT: Spellman, Michael W.
TILLE OF INVENTION: O-Fucosyltransferase
FILLE REFERENCE: Pl041PlD1-Substitute
CURRENT APPLICATION NUMBER: US/09/333,729A
CURRENT PILING DATE: 1999-06-15
PRIOR FILING DATE: 1997-11-26
SEQ ID NOS: 21
LENGTH: 365
 Sequence 6, Application US/08978741
Patent No. 6100076
GENERAL INFORMATION:
APPLICANT: Yang Wang, Michael W. Spellman
TITLE OF INVENTION: 0-Fucosyltransferase
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
 P1041P1
 PC-DOS/MS-DOS
 MEDIUS. -
COMPUTER: IBM rc CCT OCERATINES SYSTEM: PC-DOS/Ms-LC.
TANABER WinPatin (Genentech)
 Sequence 3, Application US/09333729A
Patent No. 6270987
 ATTORINY AGENT INFORMATION:
NAME: SYODOGA Craig G.
REGISTRATION UNDERER: 39,044
REFERENCE/DOCKET UNDERER: P1041
TELECOMMUNICATION INFORMATION:
TELEFONE: 650/252-1489
TELEFONE: 650/252-1489
TELEFONE: 650/252-1489
TELEFONE: 650/252-1489
TELEFONE: 650/252-1489
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TELEFONE: 650/252-1489
 Genentech, Inc.
 CITY: South San Francisco
STATE: California
COUNTRY: USA
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Best Local Similarity 91.5%;
Matches 54; Conservative
 Query Match
Best Local Similarity 91.5%;
Matches 54; Conservative
 COMPUTER READABLE FORM:
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 TYPE: PRT ORGANISM: Homo Sapien
FILING DATE: 31
 GENERAL INFORMATION:
 ADDRESSEE:
 US-09-333-729A-3
 US-09-333-729A-3
 COUNTRY:
 JS-08-978-741-6
 STREET:
 US-08-978-741-2
 RESULT 6
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 3 AGSWDLAGYLLYXPXMGRFGNQADHFLGSLAFAKLXVRTLAVPPWIEYQHHKPPFTNLH 61
 35 AGSWDPAGYLLYCPCMGRFGNQADHFLGSLAFAKLINRTLAVPPWIEYQHHKPPFTNLH 93
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 Score 295; DB 3; Length 397;
Pred. No. 2e-31;
0; Mismatches 5; Indels
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90.5%; Score 295; DB 3; Length 397;
Best Local Similarity 91.5%; Pred. No. 2e-31;
Matches 54; Conservative 0; Mismatches 5; Indels
 , OTHER INFORMATION: Plasmid insert encoded protein US-09-333-729A-7
 Sequence 17, Application US/08978741
; Patent No. 6100076
; GENERAL INFORMATION:
 APPLICANT: Yang Wang, Michael W. Spellman; TITLE OF INVENTION: O-Fucosyltransferase; NUMBER OF SEQUENCES: 17
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 1 DNA Way
 CITY: South San Francisco
 Sequence 7, Application US/09333729A
Patent No. 6270987.
GENERAL INFORMATION:
APPLICANT: Wang, Yang
APPLICANT: Spellman, Michael W.
TITLE OF INVENTION: O-Fucosyltransferase
FILE REFERENCE: 1041P101-20bstitute
CURRENT APPLICATION NUMBER: US/09/333,729A
CURRENT FILING DATE: 1999-06-15
PRIOR APPLICATION NUMBER: US 08/798,741
PRIOR FILING DATE: 1997-11-26
NUMBER OF SEQ ID NOS: 21
SEQ ID NO 7
PEDELICATION NUMBER: US/08/978,741
FILING DATE: 26-No. 6100076-1997
CLASSIPRICATION: 435
PRIOR APPLICATION NATA:
APPLICATION NUMBER: 08/792498
FILING DATE: 31
ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P1041P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
 TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
 TYPE: PRT
ORGANISM: Artificial Sequence
 Query Match 90.5%;
Best Local Similarity 91.5%;
Matches 54; Conservative
 LENGTH: 397 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
 US-09-333-729A-7
 RESULT 9
US-08-978-741-17
 US-08-978-741-6
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; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster; CIRERERNCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
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; SOFTWARE: PARTENTIN Ver. 2.0
; SEQ ID NO 45921
; LENGTH: 399
; TYPE: RRT
; CRGANISM: Drosophila melanogaster
US-09-270-767-45921
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 Length 474;
 Length 399;
 7 DLAGYLLYXPXMGRFGNQADHFLGSLAFAKLXVRTLAVPPWIEYQ 51
 25 DPNGYLTYCPCMGRFGNQADHFLGSLAFAKALNRTLILPPWVEYR 69
 / Match 35.0%; Score 114; DB 3; Length 47.
Local Similarity 64.7%; Precl. No. 4.8e-07.
Iss 22; Conservative 4; Mismatches 8; Indels
 Query Match 54.3%; Score 177; DB 4; Length 39; Best Local Similarity 73.3%; Pred. No. 1.4e-15; Matches 33; Conservative 3; Mismatches 9; Indels
 RESULT 12
US-08-978-741-8

1 Sequence 8, Application US/08978741

1 Patent No. 6100076

2 GENERAL INFORMATION:

APPLICANT: Yang Wang, Michael W. Spellman;

TITLE OF INVENTION:

ADDRESSEE: Genethech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUMPTR: USA

ZIP: 94080

COMPUTER READBLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: READBLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: READBLE FORM:

MEDIUM TYPE: 3.5 inch, 1.49 Mb floppy disk

COMPUTER: 1 MN PRE: 3.5 inch, 1.49 Mb

COMPUTER: 1 MN PRE: 3.5 inch, 1.49 Mb

SOFTWARE: WinPatin (Genentech)

CURRENT SPELICATION DATA:

APPLICATION NUMBER: US/08/978,741

FILING DATE: 3.6 NO. 610076-1997

CLASSIFICATION NUMBER: 39,044

REFERENCE/DOCKET NUMBER: 39,044

REFERENCE/DOCKET NUMBER: 39,044

REFERENCE/DOCKET NUMBER: P1041P1

TELECOMMUNICATION INFORMATION:

TELERAN: 650/25-1489

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TELERAN: 650/25-1489

TELERAN: 650/25-1489

TELERAN: 650/25-1489
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 19 GRFGNQADHFLGSLAFAKLXVRTLAVPPWIEYQH 52
 LENGTH: 474 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
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US-09-333-729A-12
 US-08-978-741-8
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 / Match 62.6%; Score 204; DB 3; Length 343; Local Similarity 94.9%; Pred. No. 2.8e-19; les 37; Conservative 0; Mismatches 2; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
DOMPUTER: IBM PC compatible
OOPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NATA:
APPLICATION NATE: 26-NO. 6100076-1997
CLASSIPTCATION 1475
PILING DATE: 26-NO. 6100076-1997
CLASSIPTCATION DATS:
APPLICATION NUMBER: 08/792498
FILING DATE: 31
APPRINCATION NUMBER: 39,044
REGISTRATION NUMBER: 19141P1
TELECHONINICATION INPORMATION:
TELEPHONE: 650/252-9881
INPORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 343 amino acids
TYPE: Amino Acid
TYPE: Amino Acid
 Sequence 13, Application US/09333729A; Sequence 13, Application US/09333729A; Patent No. 6270997; GENERAL INFORMATION:
APPLICANT: Mang.Yana.
APPLICANT: Spellman, Michael W.
TITLE OF INVENTION: O-Fucosyltransferace; TITLE REFERENCE: P1041P1D1-Substitute; CURRENT FAPLICATION NUMBER: US/09/333,729A; CURRENT FILING DATE: 1999-06-15; PRIOR PELING DATE: 1997-11-26; NUMBER OF SEQ ID NOS: 21
SEQ ID NO 13
LENGTH: 343
 Sequence 45921, Application US/09270767 Patent No. 6703491 Patent No. FORMATION: APPLICANT: Homburger et al.
 TYPE: PRT
CORGANISM: Homo Sapien
US-09-333-729A-13
 California
 US-09-270-767-45921
 Query Match
 Best Loca
Matches
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11 AGSWDPAGYLLYXPXMGR 28

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ZIP: 94080

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FILING DATE: 26-No. 6100076-1997
CLASSIFICATION NUMBER: 08/792498
FILING DATE: 31
ATTORNEY AGENT INPORMATION: NAME: SYODOGA, Craig G. REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: 39,044
REFERENCE/DOCKET NUMBER: 91041P1
TELECOMMUNICATION INPORMATION: TELECHONNE: 650/225-1489
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 US-08-17-14

Sequence 14, Application US/08978741

Sequence 14, Application US/08978741

Patent No. 6100006;

APPLICANT: Yang Wang, Michael W. Spellman

TITLE OF INVENTION: O-Fucosyltransferase

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetech, Inc.
STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA
 APPLICANT: Wang, Yang
APPLICANT: Spellman, Michael W.
TITLE OF INVENTION: O-Fucosyltransferase
FILE REPERENCE: Pl041P1D1.-Subsetitute
CURRENT PILION NUMBER: US/09/333,729A
CURRENT PILION DATE: 1999-06-15
PRIOR APPLICATION NUMBER: US 08/798,741
PRIOR PILING DATE: 1997-11-26
NUMBER OF SEQ ID NOS: 21
SEQ ID NO 12
LENGTH: 474
TYPE: PRT
CAGNOTANISM: Caenorhabditis Elegans
Sequence 12, Application US/09333729A Patent No. 6270987 GENERAL INFORMATION:
 TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
 28 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear
 US-09-333-729A-12
 US-08-978-741-14
 RESULT 14
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Gaps ö

3 AGSWDLAGYLLYXPXMGR 20

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 Length 28;
 1; Indels
 TYPE: PRT
ORGANISM: Artificial Sequence
PEATURE:
OTHER INFORMATION: Plasmid insert encoded protein.
NAME/KEY: unsure
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24.8%; Score 81; DB 3; I
Best Local Similarity 94.4%; Pred. No. 0.00048;
Matches 17; Conservative 0; Mismatches 1:
 APPLICANT: Wang, Yang
APPLICANT: Spellman, Michael W.
TITLE OF INVENTION: O-Fucosyltransferase
FILE REFERENCE: P1041PLD1-Substitute
CURRENT APPLICATION NUMBER: US/09/333,729A
CURRENT FILING DATE: 1999-06-15
FRIOR APPLICATION NUMBER: US 08/798,741
FRIOR APPLICATION DATE: 1997-11-26
NUMBER OF SEQ ID NOS: 21
SEQ ID NO 14
 Search completed: October 25, 2005, 15:42:48 Job time : 11.0205 secs
 LOCATION: 23, 25

COTHER INFORMATION: unknown amino acid

US-09-333-729A-14
US-09-333-729A-14; Sequence 14, Application US/09333729A; Sequence 100. 62709B7; Patent No. 62709B7; GENERAL INFORMATION:
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ALIGNMENTS

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Sequence 6, Appli
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GenCore version 5.1.6
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US-09-774-954-2
US-10-301-822-169
US-09-774-954-6
US-109-774-954-17
US-11-097-143-18162
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
 Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Match Length
 Title:
Perfect score:
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 Sequence:
 Searched:
 Database
 Run on:
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|                                         | GENERAL INFORMATION:                                                       |
|                                         | , APPLICANT: Yang Wang, Michael W. Spellman                                |
|                                         | ; TITLE OF INVENTION: O-Fucosyltransferase                                 |
|                                         | , NUMBER OF SEQUENCES: 17                                                  |
|                                         | ; CORRESPONDENCE ADDRESS:                                                  |
|                                         | , ADDRESSEE: Genentech, Inc.                                               |
|                                         | STREET: 1 DNA Way                                                          |
|                                         | ; CITY: South San Francisco                                                |
|                                         | ; STATE: California                                                        |
|                                         | ; COUNTRY: USA                                                             |
| - C                                     | ; ZIP: 94080                                                               |
| inted                                   | COMPUTER READABLE FORM:                                                    |
|                                         | MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk                                 |
|                                         | ; COMPUTER: IBM PC compatible                                              |
|                                         | ; OPERATING SYSTEM: PC-DOS/MS-DOS                                          |
|                                         | ; SOFTWARE: WinPatin (Genentech)                                           |
|                                         | ; CURRENT APPLICATION DATA:                                                |
| <u> </u>                                | ; APPLICATION NUMBER: US/09/774,954                                        |
| * * * * * * * * * * * * * * * * * * * * | ; FILING DATE: 30-Jan-2001                                                 |
| 3. Appli                                | ; CLASSIFICATION: <unknown></unknown>                                      |
| 9. Appli                                | PRIOR APPLICATION DATA:                                                    |
| 2. Appli                                | , APPLICATION NUMBER: US/08/978,741                                        |
| 169, App                                | FILING DATE: 26-NOV-1997                                                   |
| 6, Appli                                | , APPLICATION NUMBER: 08/792,498                                           |
| 17, Appl                                | FILING DATE: 31-JAN-1997                                                   |
| 18162, A                                | ; ATTORNEY/AGENT INFORMATION:                                              |
| 8, Appli                                | , NAME: Svoboda, Craig G.                                                  |
| 14, Appl                                | ; REGISTRATION NUMBER: 39,044                                              |
| 102, App                                | ; REFERENCE/DOCKET NUMBER: P1041P1                                         |
| 12551, A                                | ; TELECOMMUNICATION INFORMATION:                                           |

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 US-09-774-954-2
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 Length 61;
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COMPUTER READALE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: 136 finch, 1.44 Mb floppy disk COMPUTER: 18M PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Windatin (Genentech)

CURRENT APPLICATION NUMBER: US/09/774,954

FILING DATE: 30-73an-2001

FILING DATE: 26-NOV-1997

APPLICATION NUMBER: US/08/978,741

FILING DATE: 31-7AN-1997

ATTORNEY AGENT ITORORMATION:

NAME: SYODOGA, CTAIG G

REGISTRATION NUMBER: 39,044

REGISTRATION NUMBER: 39,044

REGISTRATION NUMBER: 139,044

REGISTRATION NUMBER: 130-1489
 Query Match
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Matches 61; Conservative 0; Mismatches 0;
 Sequence 9, Application US/09774954

Publication No. US20040241645A1
GENERAL OF INFORMATION:
TITLE OF INVENTION: O-Fucosyltransferase
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
 TELEFAX: 650/952-9881

TELEFAX: 650/952-9881

SEQUENCE CHARACTERISTICS:
LENGTH: 61 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 3:
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 TOPOLOGY: Linear SEQ ID NO: 9: US-09-774-954-9
 STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
 TELEPHONE: 650/225-1489
 LENGTH: 61 amino acids
TYPE: Amino Acid
 650/952-9881
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Sequence 169, Application US/10301822
Publication No. US20030148410A1
GENERAL INFORMATION:
More application No. US20030148410A1
GENERAL INFORMATION:
More applicant:
APPLICANT:
Gillemette, Allison
APPLICANT:
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APPLICANT:
Monahan, John E.
APPLICANT:
Thibodeau, Stephen N.
APPLICANT:
Thibodeau, Stephen N.
APPLICANT:
This OF INVENTION: NOTE GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: NOTE GENES, COMPOSITIONS, RISSENBUT, PREVENTION, AND
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 3 AGSWDLAGYLLYXPXMGRFGNQADHFLGSLAFAKLXVRTLAVPPWIEYQHHKPPFTNLH 61
 3 AGSWDPAGYLLYCPCMGRFGNQADHFLGSLAFAKLLNRTLAVPPWIEYQHHKPPFTNLH 61
 Query Match 90.5%; Score 295; DB 11; Length 365; Best Local Similarity 91.5%; Pred. No. 6.3e-31; Matches 54; Conservative 0; Mismatches 5; Indels (
 COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IRB PC compactable
COMPUTER: IRB PC compactable
COMPUTER: IRB PC compactable
COMPUTER: IRB PC compactable
COMPUTER: IRB PC compactable
SOFTWARE: WithDatin (Genentech)
CURRENT APPLICATION NUMBER: US/09/774,954
PILING DATE: 30-Jan-2001
CLASSIFICATION NUMBER: US/08/978,741
RILING DATE: 26-MOV-1997
RPLING DATE: 26-MOV-1997
RPLING DATE: 31-JAN-1997
APPLICATION NUMBER: 08/722,498
FILING DATE: 31-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: SVODGA, CTR-10
REFERENCE/DOCKET NUMBER: 39,044
REFERENCE/DOCKET NUMBER: 39,044
REFERENCE/DOCKET NUMBER: 19041P1
TELEPHONE: 650/225-1489
Sequence 2, Application US/09774954
Fublication No. US20040241645A1
GENERAL INFORMATION:
TITLE OF INVENTION:
OORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
DADDRESSEE: Genentech, Inc.
STREET I DNA WAY
CITY: South San Francisco
STATE: California
 TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 LENGTH: 365 amino acids
TYPE: Amino Acid
 TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
```

61

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ZIP: 94080
COMPUTER READABLE FORM:
MEDIUW TEPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/774,954
 1 NQADHFLGSLAFAKLLNRTLAVPPWIEYQHHKPPFTNLH 39
 Query Match 62.6%; Score 204; DB 11;
Best Local Similarity 94.9%; Pred. No. 9.5e-19;
Matches 37; Conservative 0; Mismatches 2;
 23 NOADHFLGSLAFAKLXVRTLAVPPWIEYQHHKPPFTNLH
 Secondary Application US/09774954
Seconder 17, Application US/09774954
Publication No. US20040241645A1
GENERAL INFORMATION:
APPLICANT: Yang Wang, Michael W. Spellman TITLE OF INVENTION: O-Fucosyltransferase NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
STREET: 1 DNA Way
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/978,741
FILING DATE: 26-NOV-1997
APPLICATION NUMBER: 08/792,498
FILING DATE: 31-JAN-1997
 P1041P1
 SEQUENCE DESCRIPTION: SEQ ID NO: 17:
 ; Sequence 18162, Application US/11097143; Publication No. US20050208558A1; GENERAL INFORMATION:
 ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P1
 CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: 60/157,832
PRIOR FILING DATE: 1999-10-05
 CITY: South San Francisco
STATE: California
 FILING DATE: 30-Jan-2001
CLASSIFICATION: <Unknown>
 TELECOMMUNICATION INFORMATION:
 TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 343 amino acids
TYPE: Amino Acid
 TELEPHONE: 650/225-1489
 COUNTRY: USA
 US-11-097-143-18162
 US-09-774-954-17
 US-09-774-954-17
 RESULT 6
 RESULT 7
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 Gaps
 26 AGSWDPAGYLLYCPCWGRFGNQADHFLGSLAFAKLLNRTLAVPPWIEYQHHKPPFTNLH
 3 AGSWDLAGYLLYXPXMGRFGNQADHFLGSLAFAKLXVRTLAVPPWIEYQHHKPPFTNLH
 ö
 Length 397;
 Query Match 90.5%; Score 295; DB 14; Length 388; Best Local Similarity 91.5%; Pred. No. 6.7e-31; Matches 54; Conservative 0; Mismatches 5; Indels (
 Indels
 ZIP: 94080

COMPUTER READABLE FORM:
COMPUTER: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech)

CURRENT APPLICATION DATA:
APPLICATION WUMBER: US/09/774,954
FILING DATE: 30-Jan-2001
CLASSIFICATION: <Unknown>
 90.5%; Score 295; DB 11;
ilarity 91.5%; Pred. No. 6.9e-31;
Conservative 0; Mismatches 5;
 Sequence 6, Application US/09774954;
Publication No. US20040241645A1
GENERAL INFORMATION:
APPLICANT: Yang Wang, Michael W. Spellman
TITLE OF INVENTION: O-Fucosyltransferase
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSE: Genentech, Inc.
STREET: 1 DNA WAY
CITY: South San Francisco
STATE: California
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/978,741
APPLING DATE: 26-NOV-1997
APPLICATION NUMBER: 08/792,498
FILING DATE: 31-JAN-1997
 PRIOR APPLICATION NUMBER: US 60/339,971
PRIOR FILING DATE: 2001-12-10
PRIOR FILING DATE: 2001-12-10
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR FILING DATE: 2002-03-05
PRIOR PILING DATE: 2002-03-05
NUMBER OF SEQ ID NOS: 228
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 169
LENGTH: 388
 ALTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: 91041P1
 TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
CURRENT APPLICATION NUMBER: US/10/301,822
 TELECOMMUNICATION INFORMATION
 TELEPHONE: 650/225-1489
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 6:
 LENGTH: 397 amino acids
 TYPE: Amino Acid
 COUNTRY: USA
 ORGANISM: Homo Sapiens
 Query Match
Best Local Similarity
Matches 54; Conserval
 US-10-301-822-169
 US-09-774-954-6
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 35 AGSWDPAGYLLYCPCMGRFGNOADHFLGSLAFAKLLNRTLAVPPWIEYQHHKPPFTNLH 93
 APPLICANT: Venter, J. Craig
APPLICANT: et al.
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
TITLE OF INVENTION: DROSOPHILA GENES.
FILE REPERENCE: CLO00728
CURRENT APPLICATION NUMBER: US/11/097,143
CURRENT FILING DATE: 2005-04-04
 Gaps
3 AGSWDLAGYLLYXPXMGRFGNQADHFLGSLAFAKLXVRTLAVPPWIEYQHHKPPFTNLH
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 Length 343;
 Indels
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Gaps
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 Length 474;
 Query Match
24.8%; Score 81; DB 11; Length 28;
Best Local Similarity 94.4%; Pred. No. 0.0021;
Matches 17; Conservative 0; Mismatches 1; Indels
 Indels
 COMPUTER READBLE PORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATURS SYSTEM: PC-DOS/MB-DOS SOFTWARE: WinPetin (Genentech)

CURRENT APPLICATION DATA: US/09/774,954

FILING DATE: 30-Jan-2001

CLASSIFICATION DATA: US/08/978,741

FILING DATE: 26-NOV-1997

APPLICATION NUMBER: US/08/978,741

FILING DATE: 31-JAN-1997

ATTOREY AGENT INFORMATION:

MAME: SYODOGA, CTAIG G

REGISTRATION NUMBER: 39,044

REFERENCE/DOCKET NUMBER: 13,0404

REFERENCE/DOCKET NUMBER: P1041P1

TELECOMUNICATION NUMBER: 39,044

REFERENCE/DOCKET NUMBER: 13,0404

TELECOMUNICATION NUMBER: 30,044

TELECOMUNICATION NUMBER: 30,044

TELECOMUNICATION INFORMATION:

TELECOMUNICATION NUMBER: 30,044

TELECOMUNICATION INFORMATION:

TELECOMUNICATION INFORMATION:

TELECHONE: 650/255-1489

TELECHONE: 650/255-1489
 RESULT 9
US-09-774-954-14

Sequence 14, Application US/09774954

Sequence 14, Application No. USZ0040241645A1

GENERAL INFORMATION:

APPLICANT: Yang Wang, Michael W. Spellman APPLICANT: Yang Wang, Michael W. Spellman CORRESPONDENCE ADDRESS:

CORRESPONDENCE ADDRESS:

ADDRESSE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA
 Query Match 35.0%; Score 114; DB 11;
Best Local Similarity 64.7%; Pred. No. 1.6e-06;
Matches 22; Conservative 4; Mismatches 8;
 19 GRFGNOADHFLGSLAFAKLXVRTLAVPPWIEYQH 52
 TOPOLOGY: Linear
;
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-774-954-14
 Sequence 102, Application US/10820474A
Publication No. US20050155089A1
GENERAL INFORMATION:
APPLICANT: LAL, PREETI
APPLICANT: TANG, Y. TOM
APPLICANT: GORGONE, GINA A.
APPLICANT: CORLEY, NEIL C.
 3 AGSWDLAGYLLYXPXMGR 20
 11 AGSWDPAGYLLYXPXMGR 28
 TYPE: Amino Acid
 RESULT 10
US-10-820-474A-102
 US-09-774-954-8
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 54.3%; Score 177; DB 20; Length 402; 73.3%; Pred. No. 4.8e-15; tive 3; Mismatches 9; Indels
 RESULT 8

US-09-774-954-8

US-09-774-954-8

Sequence 8, Application US/09774954

Publication No. US20040241645A1

Publication No. US20040241645A1

GENERAL INFORMATION: O-FUCOSYLTANSFETABLE APPLICAMY: Yang Wang, Michael W. Spellman APPLICAMY: Yang Wang, Michael W. Spellman TITLE OF INVENTION: O-FUCOSYLTANSFETABLE NOWESSEE: Genentech, Inc. STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: South San Francisco

STATE: California

CONPUTER: READABLE FORM:

MEDIUM TYPE: 35 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOSS/MS-DOS

SOFTWARE: WINPETH: GGONGALECH)

CURRENT APPLICATION DUMBER: US/09/774,954

FILING DATE: 30-Jan-2001

CLASSIFICATION NUMBER: US/08/791,498

FILING DATE: 31-JAN-1997

ATTORNEY APPLICATION NUMBER: 08/792,498

FILING DATE: SYONOV-1997

ATTORNEY/AGENT INFORMATION:

NAME: SYODOGA, Crair CRAIRCANTION:

NAME: SYODO
 28 DPNGYLTYCPCMGRFGNQADHFLGSLAFAKALNRTLILDPPWVEYR 72
 7 DLAGYLLYXPXMGRFGNQADHFLGSLAFAKLXVRTLAVPPWIEYQ 51
PRIOR APPLICATION NUMBER: 60/160,191
PRIOR FILING DATE: 1999-10-19
PRIOR FILING DATE: 1999-10-19
PRIOR FILING DATE: 1999-10-28
PRIOR FILING DATE: 1999-11-2
PRIOR APPLICATION NUMBER: 60/164,769
PRIOR FILING DATE: 1999-11-12
PRIOR FILING DATE: 1999-11-28
PRIOR FILING DATE: 2000-01-12
PRIOR FILING DATE: 2000-01-12
PRIOR PRILING DATE: 2000-02-44
PRIOR FILING DATE: 2000-02-34
PRIOR FILING DATE: 2000-03-33
PRIOR PRILING DATE: 2000-03-33
NUMBER OF SEQ ID NOS: 43008
SOFTHARRE: FastSEQ for Windows Version 4.0
LENGTH: 402
 NAME: Svoboda, Craig G.
REGIGFRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P1041P1
TELECOMMUNICATION INFORMATION:
 TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
 INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 474 amino acids
TYPE: Amino Acid
 Query Match
Best Local Similarity 73.3%
Marches 33, Conservative
 ORGANISM: DROSOPHILA
 US-11-097-143-18162
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APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas A.
APPLICANT: Sovalic, David K.
APPLICANT: Shou, Yihua
APPLICANT: Shou, Yihua
APPLICANT: Or INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REPERENCE: 38-21 (5)222) B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 201329
LENGTH: 189
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 60 SWDIKNY-LWAPRLGMYGIQRIHLLGNVMVLAGAGVGGGSLNYA----NTLYVPPKAFFD 114
 46
 TITLE OF INVENTION: Identification of Essential Genes in Microorganisms FILE REFERENCE: ELITRA.034A CURRENT APPLICATION NUMBER: US/10/282,122A CURRENT FILING DATE: 2003-02-20
 GSLAFAKLXVRTLAVPP----
 1 RLAGSWDLAGY--LLYXPXMGRFGNQADHFLGSLAFAKLXVRTLAVPPWIEYQHH 53
 s.
 Query Match 21.9%; Score 71.5; DB 16; Length 189; Best Local Similarity 40.0%; Pred. No. 0.3; Matches 22; Conservative 4; Mismatches 24; Indels 5
 ; OTHER INFORMATION: Clone ID: MRT4577_115198C.1.pep
US-10-425-115-201329
 PRIOR APPLICATION NUMBER: 00/10/282,1
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR PLILING DATE: 2000-05-23
PRIOR PLILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-6
PRIOR FILING DATE: 2000-05-6
PRIOR FILING DATE: 2000-05-6
PRIOR FILING DATE: 2000-05-6
PRIOR FILING DATE: 2000-05-6
PRIOR FILING DATE: 2000-05-6
PRIOR FILING DATE: 2000-05-6
 Sequence 201329, Application US/10425115 Publication No. US20040214272A1 GENERAL INFORMATION:
 Sequence 61790, Application US/10282122A
Publication No. US20040029129A1
 5 SWDLAGYLLYXPXMGRFGNQADHFL
 115 DPOWKDITDWÓEELKÞY 131
 47 ---W---IEYQHHKPPF 57
 APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
 nd, Judith
Daniel
ck, John
 Carr, Grant
Yamamoto, Robert
Forsyth, R.
 Trawick,
 TYPE: PRT
ORGANISM: Zea mays
 GENERAL INFORMATION:
 RESULT 12
US-10-425-115-201329
 US-10-282-122A-61790
 APPLICANT:
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 Indels 29;
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 22.2%; Score 72.5; DB 14; Length 601; 29.9%; Pred. No. 0.77; tive 8; Mismatches 17; Indels 29.
 Query Match 23.3%; Score 76; DB 18; Length 150; Best Local Similarity 77.8%; Pred. No. 0.059; Matches 14; Conservative 1; Mismatches 3; Indels
 APPLICANT: REDDY, ROOPA
APPLICANT: HELMAN, JENNIFER L.
APPLICANT: HILMAN, JENNIFER L.
APPLICANT: HILMAN, JENNIFER L.
TITLE OF INVENTION: SIGNAL PEPTIDE-CONTAINING MOLECULES
TITLE OF INVENTION: SIGNAL PEPTIDE-CONTAINING MOLECULES
TITLE OF INVENTION: SIGNAL PEPTIDE-CONTAINING MOLECULES
CURRENT TILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: 09/720,533
PRIOR FILING DATE: 1099-06-25
PRIOR PELICATION NUMBER: 60/090,762
PRIOR PELICATION NUMBER: 60/094,983
PRIOR FILING DATE: 1998-06-25
PRIOR FILING DATE: 1998-07-31
PRIOR FILING DATE: 1998-07-31
PRIOR FILING DATE: 1998-10-01
SHOR APPLICATION NUMBER: 60/102,686
PRIOR FILING DATE: 1998-07-31
PRIOR FILING DATE: 1998-07-31
SEQ ID NOS: 269
SOFTWARE: PALENTIN VERSION 3.3
SEQ ID NO 102
LENGTH: 150
 FEATURE:
NAME/KEX: misc_feature
THER INFORMATION: Incyte Clone No: 1647884
US-10-820-474A-102
 APPLICANT: OWURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: BHIRAWA, JUN
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: HATTORI MASAHIRA
ITILE OP INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-39
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-05-30
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 12551
 Sequence 12551, Application US/10156761 Publication No. US20030119018A1 GENERAL INFORMATION:
 ; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-12551
 3 AGSWDLAGYLLYXPXMGR 20
 26 AGSWDPAGYLLYCPCMGK 43
GUEGLER, KARL J.
BAUGHN, MARIAH R.
AKERBLOM, INGRID E.
AU-YOUNG, JANICE
YUE, HENRY
PATTERSON, CHANDRA
 Query Match 22.2
Best Local Similarity 29.9
Matches 23; Conservative
 ORGANISM: Homo sapiens
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 RESULT 14
19-10-424-599-266118
Sequence 266118, Application US/10424599
Publication No US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Cao Yongwei
TITLE OF INVENTION: SOY Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: SOY Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: 920 Nucleic Acid Molecules Associated With
TITLE OF INVENTION: 804 Nucleic Acid Molecules Associated With
TITLE OF INVENTION: 0216322)B
CURRENT APPLICATION UNMERS: uS/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 266118
 Ξ,
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR PILLING DATE: 2000-10-23
PRIOR FILLING DATE: 2000-11-27
PRIOR PRILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/267,931
PRIOR PILLING DATE: 2001-2-22
PRIOR PAPLICATION NUMBER: 60/269,308
PRIOR PILLING DATE: 2001-02-09
PRIOR FILLING DATE: 2001-02-09
PRIOR FILLING DATE: 2001-02-16
NUMBER: OF SEQ ID NOS: 78614
SEQ ID NOS: 78614
SEQ ID NO 61790
LENGTH: 198
 Gaps
 3; Gaps
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 Ouery Match
Best Local Similarity 37.2%; Pred. No. 0.61;
Matches 16; Conservative 7; Mismatches 17; Indels 3
 Length 198;
 Query Match
21.3%; Score 69.5; DB 15; Length 19
Best Local Similarity 50.0%; Pred. No. 0.59;
Matches 16; Conservative 2; Mismatches 11; Indels
 11 YLLYXPXMGRFGNQADHFLGSLAFAKLXVRTLAVPPWIEYQHH 53
 ; OTHER INFORMATION: Clone ID: PAT_MRT3847_82325C.1.pep
US-10-424-599-266118
 TYPE: PRT
ORGANISM: Glycine max
PERJURE:
NAME/KEY: unsure
LOCATION: (1)..(152)
PERJURE:
PERJURE:
 21 FGNOADHFLGSLAFAKLXVRTLAV---PPWIE 49
 Sequence 113919, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
 ; TYPE: PRT
; ORGANISM: Mycobacterium avium
US-10-282-122A-61790
 RESULT 15
US-10-437-963-113919
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APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Pingl
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 1 RLAGSWDLAG--YLLYXPXMGRFGNQADHFLGSLAFAKLXVRTLAVPPWIEYQHH 53
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20.7%; Score 67.5; DB 16; Length 538;
Best Local Similarity 38.2%; Pred. No. 3.2;
Matches 21; Conservative 5; Mismatches 24; Indels 5;
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US-10-437-963-113919
 Search completed: October 25, 2005, 15:41:23 Job time : 37.8234 secs
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 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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XX Alschul S.F., Teingold E.A., Grouse L.H., Derge J.G.,

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XX Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

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XX Raha S.S., Loqquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

XX Bana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

XX Robert S.J., McEwan P.J., McKernan K.J., Malek J.A., Gubarathe P.H.,

XX Norley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

XX Vilalano D.K., Muzny D.M., Sodergen B.J., Lu X., Gibbs R.A.,

XX Nilalan M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

XX Niting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

XX Niting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

XX Butterfield Y.S.N., Krzywinski M.I., Skalius D.E.,

XX Schnerch A., Schein J.E., Jones S.J.W., Marra M.A.;

XX Generation and initial analysis of more than 15,000 full-length human
Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J., A Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D., Kay M.P., Kimberley A.M., King A., Knigtes A., Laird G.K., Lawlor B., Lehvaeslaiho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D., A Lehvaeslaiho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D., Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McMurray A.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T., Oliver K., Parker A., Patel R., Pearca T.A.V. Peck A.I., A Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H., Rice C.M., Ross M.T., Socht C.E., Shra H.K., Shownkeen R., Sims S., Skun R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A., Tracey A., Tromans A.C., Vaudin M., Wallis J.M., Thorpe A., Mhitchead S.L., Whittaker P., Willey D.L., Williams S.A., Milming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S., Rocers J.:
 "The DNA sequence and comparative analysis of human chromosome 20."; Nature 414:865-871(2001).
 SEQUENCE FROM N.A. (ISOFORM 2).
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 MEDIATE-9175972; PubMed=9023546;
MEDIATE-97175972; PubMed=9023546;
MEDIATE-97175972; PubMed=9023546;
MEDIATE-97175972; Relley R.E., Spellman M.W.;
Mang Y., Lee G.F., Kelley R.E., Spellman M.W.;
"Identification of a GDP-L-fucose:polypeptide fucosyltransferase and enzymentic addition of 0-linked fucose to EGF domains.";
-I-FUNCTION: Catalyzes the reaction that attaches fucose through an O-glycobidic linkage to a conserved serine or threonine residue in EGF domains
-I-CATALYTIC ACTIVITY: Transfers an alpha-L-fucosyl residue from GDP-beta-L-fucose to the serine hydroxy group of a protein acceptor.
-I-COPACTOR: Mangannese.
-I-PATHWAY: Glycosylation.
 IsoId=Q9H488-2; Sequence=VSP_001809;
Note=No experimental confirmation available;
Note=No experimental confirmation available;
-!-TISSUE SPECIFICTIY: Highly expressed in heart, brain, placenta, lung, liver, skeletal muscle, kidney and pancreas.
-!- SIMILARITY: Belongs to the glycosyltransferase 68 family.
and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 Event=Alternative splicing; Named isoforms=2;
 IsoId=Q9H488-1; Sequence=Displayed;
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 PubMed=12966037; DOI=10.1093/glycob/cwg113;
PubMed=12966037; DOI=10.1093/glycob/cwg113;
Martinez-Duncker I., Mollicone R., Candelier J.J., Breton C.,
Martinez-Duncker I., Mollicone R., Candelier J.J., Breton C.,
Oriol R.;
"A new superfamily of protein-0-fucosyltransferases, alpha?-
"A new superfamily of protein-0-fucosyltransferases; phylogeny and
identification of conserved peptide motifs.",
Glycobiology 13:10-55(2003)
-1- FUNCTION: Catalyzes the reaction that attaches fucose through an
0-glycosidic linkage to a conserved serine or threonine residue in
ESF domains (By similarity).
-1- CATALYTIC ACTIVITY: Transfers an alpha-L-fucosyl residue from GDP-
beta-L-fucose to the serine hydroxy group of a protein acceptor.
 N-linked (GlCNAC.) (Potential).

FSPKEHPVLALPGARACFPVLEHRPLOKYMYWSDBNVKTG
BAQIHAHLVRPYVGIHLRIGSDWKNACAMLKDGTAGSHFWA
SPQCYVSTRSTRALPLTHWALDEDLEETORAVMYNBELDAG
SVYVATOSESYPELQQLFKGRVKVVSLKFBVYQLDYILLEQ
QADHFIGNUSSFTARVKREDLQGRFSSFFGMDRPFKLRD
FF - RENHSCYTLLFPR (in isoform 2).

FFILd=YSP_001809.
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25-0CT-2004 (Rel. 45, Last sequence update)
25-0CT-2004 (Rel. 45, Last sequention update)
25-0CT-2004 (Rel. 45, Last annotation update)
CDP-fucose protein O-fucosyltransferase 1 precursor (EC 2.4.1.221)
Name=POFUTL; Synonymes=Furl2;
Pan troglodytes (Chimpanzee);
Pan troglodytes (Chimpanzee)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Nammalia; Euheria; Primates; Catarrhini; Hominidae; Pan.
 R GNOS 14989; POFUTI.

R HINOUB; HIXOUIS724;
HINOUB; HIXOUIS724;
HINOUB; HIXOUIS724;

R GO; GO: 0005737; C:cytoplasm; ISS.
R GO; GO: 0005737; C:cytoplasm; ISS.
R GO; GO: 0005737; C:cytoplasm; ISS.
R GO; GO: 0005739; P:embryonic development; NAS.
R GO; GO: 0005739; P:embryonic development; NAS.
R GO; GO: 0005739; P:embryonic development; NAS.
R GO; GO: 0005449; P:regulation of transcription; NAS.
R GO; GO: 0006449; P:regulation of transcription; NAS.
R GO; GO: 0006449; P:regulation of translation; NAS.
R GO: 0006449; P:regulation of translation; NAS.
R GO: 0006449; P:regulation of translation; NAS.
R GO: 0006
 N-linked (GlcNAc. . .) (Potential).
 Query Match
Best Local Similarity 100.0%; Pred. No. 4.5e-36;
Matches 61; Conservative 0; Mismatches 0; Indels 0
 SEQUENCE 388 AA; 43955 MW; 3FACCCA434D02415 CRC64;
 PRT; 388 AA.
 EMBL, AF375884; AAL09576.1; -. EMBL, B08002; BAA11497.2; -. EMBL, AL121897; CAC16424.1; -. EMBL, BC000582; AAH00582.1; -.
 STANDARD;
 61 H 61
 84 H 84
 OFUL PANTR
Q6EV69;
 CARBOHYD
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 RESULT 2
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Loriol C., Germot A., Dupuy F., Maftah A.;
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, A7344580; AAQ02332.1; -.
GO; GO:0016757; Frtransferase activity, transferring glycosyl. . .; IEA.
GLycosyltransferase; Transferase.
SEQUENCE 391 AA; 44307 MW; 96762ABB1A2027AD CRC64;
 27 LPVGSWDPAGYLLYCPCMGRFGNQADHFLGSLAFAKLINRTLAVPPWIEYQHHKPPFTNV
 1 MPAGSWDPAGYLLYCPCMGRFGNQADHFLGSLAFAKLLNRTLAVPPWIEYQHHKPPFTNL
 Bos taurus (Bovine).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
 ch 97.2%; Score 343; DB 2; Length 391; I Similarity 95.1%; Pred. No. 8.4e-35; 58; Conservative 2; Mismatches 1; Indels
 Last sequence update)
Last annotation update)
391 AA
 Protein-O-fucosyltransferase (Fragment)
 Created)
PRT;
 PRT;
 01-0CT-2003 (TrEMBLrel. 25, Creat
01-0CT-2003 (TrEMBLrel. 25, Last
01-MAR-2004 (TrEMBLrel. 26, Last
Protein O-fucosyltransferase la.
Name-pofuti;
 PRELIMINARY;
PRELIMINARY;
 378
 Local Similarity
 Best Local Similarity
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 NCBI_TaxID=9913;
 61 H 61
 61 H 61
 87 H 87
 Bovinae; Bos.
 Name=POFUT1;
 SEQUENCE
 Query Match
 Query Match
 NON TER
NON TER
 07YRZ3;
 27YRE7
 Q7YRZ3
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 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
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 1 MPAGSWDPAGYLLYCPCMGRFGNQADHFLGSLAFAKLLNRTLAVPPWIEYQHHKPPFTNL 60
 1 MPAGSWDPAGYLLYCPCMGRFGNQADHFLGSLAFAKLLNRTLAVPPWIEYQHHKPPFTNL 60
 24 MPAGSWDPAGYLLYCPCMGRFGNQADHFLGSLAFAKLLNRTLAVPPWIEYQHHKPPFTNL 83
 0; Gaps
 Gaps
 GDP-fucose protein O-fucosyltransferase
 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
 EMBL; AJ781500; CAH03712.1; -.
Fucose metabolism; Glycoprotein; Glycosyltransferase; Manganese; Signal; Transferase.
Signal, Transferase.
SIGNAL
 Loriol C., Germot A., Dupuy F., Maftah A.;
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AY344581; AA02233.1; --
EMBL, AY344581; AA02233.1; --
EMBL, EMBL, Transferase activity, transferring glycosyl.
Glycosyltransferase; Transferase.
SEQUENCE 351 AA; 39576 MW; BF830F61A7296F42 CRC64;
 N-linked (GlCNAc. . .) (Potential).
N-linked (GlCNAc. . .) (Potential).
3FACCCA434D02415 CRC64;
 ;
0
 -i- PATHWAY: Glycosylation.
-i- SIMILARITY: Belongs to the glycosyltransferase 68 family.
 ; Score 353; DB 1; Length 388; ; Pred. No. 4.5e-36; 0; Mismatches 0; Indels
 97.2%; Score 343; DB 2; Length 351; 95.1%; Pred. No. 7.5e-35; tive 2; Mismatches 1; Indels
 Last sequence update)
Last annotation update)
 351 AA
 COFACTOR: Manganese (By similarity)
 01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last seq
01-MAR-2004 (TrEMBLrel. 26, Last ann
 PRT;
 Protein O-fucosyltransferase 1b.
 62 62 N
160 160 N
388 AA; 43955 MW;
 Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 61; Conservative 0,
 Query Match
Best Local Similarity 95.1.
Best Local Similarity 95.1.
 PRELIMINARY;
 SEQUENCE FROM N.A.
 NCBI_TaxID=9913;
 87 H 87
 84 H 84
 61 H 61
 61 H 61
 Name=pofut1;
 CARBOHYD
CARBOHYD
 SEQUENCE
 Q7YRE6;
 Q7YRE6
 CHAIN
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RESULT 3

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 1 MPAGSWDPAGYLLYCPCMGRFGNQADHFLGSLAFAKLLNRTLAVPPWIEYQHHKPPFTNL 60
 20 LPAVSWDPAGYLLYCPCMGRFGNQADHFLGSLAFAKLLNRTLAVPPWIEYQHHKPPFTNL 79
 Martinez-Dunker II., Mollicone R., Candelier J.J., Breton C., Oriol R.; Martinez-Dunker II., Mollicone R., Candelier J.J., Breton C., Oriol R.; "A new superfamily of protein-0-fucosyltransferases, alpha2-fucosyltransferases, and alpha6-fucosyltransferases; phylogeny and identification of conserved peptide motifs."; Glycobiology 13:1C-5c(2003). Glycobiology 13:1C-5c(2003). Glycobiology Glycobyltransferase activity, transferring glycosyl. .; IEP Glycosyltransferase; Transferase.
 0; Gaps
 Sus scrofa (Pig).
Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
NCBI_TaxID=9823;
 ch 96.6%; Score 341; DB 2; Length 378; I Similarity 96.7%; Pred. No. 1.5e-34; 59; Conservative 1; Mismatches 1; Indels
 378 AA; 42842 MW; 1870DEB0C50713F1 CRC64;
 01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
378 AA.
 80 H 80
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RESULT Q7YRE7

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Q8C8R4
 CHAIN
 RESULT 7
Q8C8R4
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 RN SEQUENCE FROM N.A.

RC STRAINE-TSUB-Mammary gland;

RX Alausner FVB/N.3; TISSUB-Mammary gland;

RATAINE-1238825; PubMed=12477932; DOI=10.1073/pnas.242603899;

RATAINE-1238825; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Altausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Altschul S.F., Loquellano W.P., Paramer C.F., Bhat N.K.,

RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Rohads S., Worley K.C., Hale S., Garcia A.M., Gab L.J., Hulyk S.W.,

RA Vilalon D.K., Muzny D.M., Gacergren B.J., Lu X., Gibbs R.A.,

RA Vilalon D.K., Muzny D.M., Gacergren B.J., Lu X., Gibbs R.A.,

RA VILALON E., Ketteman M., Madan A.M., Gabbs R.A.,

RA Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Hakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Bakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butcerfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butcerfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butcerfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

C. - CHNCTION: Catalyzes the reaction that attaches fucose through an O-glycosidic linkage to a conserved serine or threonine residue in

C. - CATALYTIC ACTIVITY: Transfers an alpha-L-fucosyl residue from C.

- COPACTOR: Mangarnes (By similarity).

C. - COPACTOR: Mangarnes (By similarity).

C. - COPACTOR: Mangarnes (By similarity).

C. - CHIMMARITY: Belongs to the glycosyltransferse 68 family.
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 SEQUENCE FROM N.A.
SARANN-1205/SvJ, TISSUB-Liver,
MEDIINE-21529/55; PubMed=11524412; DOI=10.1074/jbc.MI07849200;
Mang Y., Shao L., Shi S., Harris R.J., Spellman M.W., Stanley P.,
Wang Y., Shao E., Shi S., Harris R.J., Spellman M.W., Stanley P.,
"Halthangarg R.S.",
"Modification of epidermal growth factor-like repeats with O-fucose:
molecular cloning and expression of a novel GDP-fucose protein O-
 28-FEB-2003 (Rel. 41, Last sequence update)
25-607-2004 (Rel. 45, Last annotation update)
GDP-fucose protein O-fucosyltransferase 1 precursor (EC 2.4.1.221)
(Peptide O-fucosyltransferase) (O-FucT-1).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI TaxID=10090;
 EMBL, AR375885, AAL09577.1; -.
EMBL, BCG64295, AAH462951; -.
MGD, MGI.2153207, Pofttl.
GO; GO:0030173; C:integral to Golgi membrane; ISS.
GO; GO:008417; F:fucosyltransferase activity; ISS.
GO; GO:0001525; P:angiogenesis; IMP.
GO; GO:0001525; P:eart development; IMP.
 393 AA
 fucosyltransferase.";
J. Biol. Chem. 276:40338-40345(2001).
 PRT;
 (Rel. 41, Created)
 STANDARD;
 Mus musculus (Mouse)
RESULT 6
OFUL MOUSE
ID OFUL MOUSE
Q91ZW2;
 28-FEB-2003
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.;
0
 61
 89
 [4]
STRAIN-CS7BL/6J; TISSUE-Retina;
STRAIN-CS7BL/6J; TISSUE-Retina;
MEDLINE-20499374; PubMed=11042159; DOI=10.1101/GF.145100;
MEDLING: P. Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Maramatsu M., Hayashizaki Y.;
Konno H., Okazaki Y., Maramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
 SEQUENCE FROM N.A.
TRAIN-CSTBIL/6J; TISSUE-Retina;
The FAWTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
than RIKEN of the mouse transcriptome based on functional annotation of
60,770 full-length oDNAs.";
 SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STAINLS-CSTDL/64; TISSUB-Retina;
MEDLINE-99279253; PubMed-10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
 Gaps
 01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Mus musculus adult train cDNA, RIKEN full-length enriched library,
clone:A930026F21 product:protein O-fucosyltransferase 1, full insert
 GDP-fucose protein O-fucosyltransferase
 SEQUENCE FROM N.A.
STRAIN-CSTBL/G1 TISSUE-Retina;
MEDLINE-20530913; PLUDMed-11076861; DOI-10.1101/gr.152600;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
 SEQUENCE FROM N.A.
STRAN-627BL/61; TISSUE-Retina;
STRAN-637BL/64; TISSUE-Retina;
MEDLINE-21085660; PubMed=11217851; DOI=10.1038/35055500;
RIKEN FANTOM CONSOCTIUM;
"Functional annotation of a full-length mouse cDNA collection.";
"Reture 409:685-690(2001).
 67 67 N-linked (GlcNAc. .) (Potential).
165 165 N-linked (GlcNAc. .) (Potential).
393 AA, 44688 MW, D982104E95E5CF3B CRC64;
GO; GO:0007399; P:neurogenesis; IMP.
GO; GO:00071219; P:Notch signaling pathway; IMP.
GO; GO:0006493; P:O-linked glycosylation; ISS.
GO; GO:0001756; P:somitogenesis; IMP.
Fuccos metabolism; Glycoprotein; Glycosyltransferase; Manganese; Signal; Transferase.
I 30 Potential.
 ..
 Length 393;
 Score 331; DB 1; Length 39
Pred. No. 2.8e-33;
0; Mismatches 1; Indels
 393 AA.
 PRT;
 ch 93.8%;
1 Similarity 98.3%;
58; Conservative
 Nature 420:563-573(2002).
 PRELIMINARY;
 30
393
 31
 CARBOHYD
SEQUENCE
 Query Match
Best Local S:
Matches 58
 CARBOHYD
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RESULT 10
Q8AWB4
 Matches
 RESULT 9
 Q6EV66
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Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
Adachi J., Aizawa K., Akimura T., Hara A., Hashizume W.,
Antuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
Antuda S., Furuno M., Hiramoto K., Hiraoka T., Hirozane T.,
Antuda K., Indini Y., Itoh M., Kagawa I., Kasukawa T.,
Antura C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
Satio R., Saitoh H., Sakai C., Sakai K., Sakzume N., Sano H.,
Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
Tagawa A., Takahshi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
 31 AGSWDLAGYLLYCPCWGRPGNQADHFLGSLAFAKLINRTLAVPPWIEYQHHKPPFTNLH 89
 61
 Gaps
 Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
 3 AGSWDPAGYLLYCPCMGRFGNQADHFLGSLAFAKLLNRTLAVPPWIEYQHHKPPFTNLH
Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watshiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y., "RIKEN integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
 "A new superfamily of protein-O-fucosyltransferases, alpha2-fucosyltransferases and alpha6-fucosyltransferases: phylogeny and identification of conserved peptide motifs.";
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 PubMed=12966037; DOI=10.1093/glycob/cwg113;
Martinez-Duncker I., Mollicone R., Candelier J.J., Breton C.,
 Length 393;
 Score 331; DB 2; Length 35
Pred. No. 2.8e-33;
0; Mismatches 1; Indels
 Martinez-Duncker I., Oriol R., Mollicone R.;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
 44704 MW; 1CA94CB30B85D6DC CRC64;
 Last sequence update)
Last annotation update)
 GO:0007399; P:neurogenesis; IMP.
GO:0007219; P:Notch signaling pathway; IMP.
GO:0001756; P:somitogenesis; IMP.
 395 AA.
 , MGI:2153207; Pofutl.
GO:0005615; C:extracellular space; TAS.
GO:0001525; P:angiogenesis; IMP.
GO:0006004; P:fucose metabolism; TAS.
GO:0007507; P:heart development; IMP.
 25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last seq
25-OCT-2004 (TrEMBLrel. 28, Last ann
Protein-O-fucosyltransferase 1.
 PRT;
 Glycosyltransferase, Transferase.
 93.8%;
98.3%;
 Query Match
Best Local Similarity 98.39
 PRELIMINARY;
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 NCBI TaxID=10116;
 STRAIN=Wistar;
 STRAIN=Wistar;
 Name=fut12;
 Oriol R.;
 SEQUENCE
 Q6EV70
 06EV70
 RESULT 8
 QEEV70
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 1 MPAGSWDPAGYLLYCPCMGRFGNQADHFLGSLAFAKLLNRTLAVPPWIEYQHHKPPFTNL 60
 98
 SEQUENCE FROM N.A.
Martinez-Duncker I., Oriol R., Mollicone R.;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ781503; CAH03714.1; -.
GO, GO:0016757; F:transferase activity, transferring glycosyl. . .; IEA.
EMBL; AJ781499; CAH03711.1; -.
GO; GO:0016757; F:transferase activity, transferring glycosyl. . .; IEA
Glycosyltransferase; Transferase.
SEQUENCE 395 AA; 44983 WW; 2A85521E22738920 CRC64;
 4 GSWDPAGYLLYCPCMGRFGNQADHFLGSLAFAKLLNRTLAVPPWIEYQHHKPPFTNLH 61
 34 GSWDLAGYLLYCPCMGRFGNQADHFLGSLAFAKLLNRTLAVPPWIEYQHHKPPFTNLH 91
 27 LPVGSWNPAGYLLFCPCMGRFGNQADHFLGSLAFAPLMNRTLAVPPWIEYQHHKPPFTNV
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 Gaps
 Gaps
 "A new superfamily of protein-O-fucosyltransferases, alpha2-fucosyltransferases: phylogeny and identification of conserved peptide motifs.";
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 ;
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 PubMed=12966037; DOI=10.1093/glycob/cwg113;
Martinez-Duncker I., Mollicone R., Candelier J.J., Breton C.,
 Score 326; DB 2; Length 391;
Pred. No. 1.2e-32;
 92.6%; Score 327; DB 2; Length 395; 98.3%; Pred. No. 9e-33; ive 0; Mismatches 1; Indels
 2; Indels
 44277 MW; 4E047D6BB5CDF7FA CRC64;
 Last sequence update)
Last annotation update)
 Last sequence update)
Last annotation update)
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 380 AA
 ch 92.4%; Score 326; DB
1 Similarity 88.5%; Pred. No. 1.2e
54; Conservative 5; Mismatches
 391
 25-OCT-2004 (TrEMBLrel. 28, Created) 25-OCT-2004 (TrEMBLrel. 28, Last seq 25-OCT-2004 (TrEMBLrel. 28, Last ann
 Created)
 PRT;
 Glycosyltransferase; Transferase
 Protein-O-fucosyltransferase 1.
 01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, Hypothetical protein POFUTI.
 57; Conservative
 PRELIMINARY;
 PRELIMINARY;
 Bos taurus (Bovine)
 391 AA;
 Query Match
Best Local Similarity
 Local Similarity
 SEQUENCE FROM N.A.
 Gallus.
NCBI_TaxID=9031;
 NCBI_TaxID=9913;
 61 H 61
 87 H 87
 Bovinae; Bos
 Name=fut12;
 Oriol R.;
 SEQUENCE
 Query Match
 Q8AWB4;
 Qeevee
Qeevee;
 Q8AWB4
 Best Loca
Matches
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SEQUENCE
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 Query Match
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 Q7T028
Q7T028;
 Best Loca
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 RESULT 12
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 18 AGSWDTAGYLLYCPCMGRFGNQAEHFLGALAFARALMRTLAVPPWIEYRHHRPPYTNLH 76
 3 AGSWDPAGYLLYCPCMGRFGNQADHFLGSLAFAKLLNRTLAVPPWIEYQHHKPPFTNLH 61
 MEDLINE-93364082, PubMed-8358148;
Harris R.J., Spellman M.W.;
"O-linked fuces and other post-translational modifications unique to
 MEDLINE=21523965; PubMed=11524432; DOI=10.1074/jbc.M107849200; MEDLINE=21523965; Alang Y., Shao L., Shi S., Harris R.J., Spellman M.W., Stanley P., Haltiwanger R.S.; Modification of epidermal growth factor-like repeats with O-fucose: molecular cloning and expression of a novel GDP-fucose protein O-fucosyltransferase."; J. Biol. Chem. 276:40338-40345(2001).
 MEDLINE-97175972; PubMed-9023546; Wang Y., Lee G.F., Kelley R.F., Spellman M.W.; "Identification of a GDP-L-fucose:polypeptide fucosyltransferase and enzymetic addition of 0-linked fucose to EGF domains."; Glycobiology 6:837-842(1996).
 0; Gaps
 25-OCT-2004 (Rel. 45, Created)
25-OCT-2004 (Rel. 45, Last sequence update)
25-OCT-2004 (Rel. 45, Last sequence update)
35-OCT-2004 (Rel. 45, Last annotation update)
GDP-fucose protein O-fucosyltransferase 1 (BC 2.4.1.221) (Peptide fucosyltransferase) (O-FucT-1) (Fragment).
 Cricetulus griseus (Chinese hamster).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalla; Butheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
Cricetulus.
 th 87.3%; Score 308; DB 2; Length 380; Similarity 86.4%; Pred. No. 2.2e-30; 51; Conservative 6; Mismatches 2; Indels
 Oriol R.; Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases. EMBL, AJ535754; CAD59738.1; -. Hypothetical protein. SEQUENCE 380 AA; 43316 MW; 83B53B342511811B CRC64;
 61 AA.
 PRT;
 EGF modules.";
Glycobiology 3:219-224(1993).
 FUNCTION, AND GLYCOSYLATION.
FISSUE=Ovary;
 STANDARD;
 Local Similarity
[1]
SEQUENCE FROM N.A.
 NCBI_TaxID=10029;
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 3 AGSWDPAGYLLYCPCMGRFGNQADHFLGSLAFAKILNRTLAVPPWIEYQHHKPPFTNLH 61
 TISSUB=Embryo;

PubMed=12477932, DOI=10.1073/pnas.242603899;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Alschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatcheho, L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 01-007-2003 (TrEMBLrel. 25, Created)
01-007-2003 (TrEMBLrel. 25, Last sequence update)
01-007-2003 (TrEMBLrel. 25, Last sequence update)
01-007-2004 (TrEMBLrel. 26, Last annotation update)
01-007-2004 (TrEMBLrel. 26, Last annotation update)
01-007-2004 (TrEMBLrel. 26, Last annotation update)
03-007-2004 (TrEMBLrel.)
04-007-2004 (EC 2.4.1.221).
04-007-2004 (TrEMBLrel.)
05-007-2004 (TrEMBLrel.)
06-007-2004 (TrEMBLrel.)

 Gaps
 3 AGSWDLAGYLLYXPXMGRFGNQADHFLGSLAFAKLXVRTLAVPPWIEYQHHKPPFTNLH
 Gaps
 25-0CT-2004 (TERMBLrel. 28, Created)
25-0CT-2004 (TERMBLrel. 28, Last sequence update)
25-0CT-2004 (TERMBLrel. 28, Last amotation update)
Hypothetical protein.
Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea; Pipidae;
 GUTENCE FROM N.A.

SEQUENCE FROM N.A.

Martinez Duncker I., Mollicone R., Candelier J.J., Breton C., Oriol R.;

Oriol R.;

Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.

EMBL: AJ579536; CAE18459.1; t.

ZFIN: ZDB-GENRE-040303-2; pofult.

ZFIN: ZDB-GENRE-040303-2; pofult.

GO; GO:0016522; P:peptide-O-fucosyltransferase activity; IEA.

GO; GO:0016757; F:transferase activity, transferring glycosyl.

Glycosyltransferase; Transferase.

SEQUENCE 395 AA; 45165 MW; 158BE06172542EBA CRC64;
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Direct protein sequencing; Fucose metabolism; Glycoprotein; Glycosyltransferase; Manganese; Transferase.
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 ch 83.6%; Score 295; DB 1; Length 61
1 Similarity 91.5%; Pred. No. 1.5e-29;
54; Conservative 0; Mismatches 5; Indels
 61 61
61 AA; 6951 MW; E9507AE60018F23A CRC64;
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 380 AA
 PRT;
 PRELIMINARY;
 PRELIMINARY;
 Aenopodinae; Xenopus.
NCBL TaxID=8364;
 SEQUENCE FROM N.A.
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Query Match
 Matches
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 Martinez-Duncker I., Mollicone R., Candelier J.J., Oriol R.;
Murtinez-Duncker I., Mollicone R., Candelier J.J., Oriol R.;
Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AdG06070; CAE54305.1; -.
GO; GO:0016757; Fitransferase activity, transferring glycosyl. ..; IEA.
InterPro; IPR000886; ER target S.
PROSITE; PS00014; ER TARGET; UNKNOWN_I.
Glycosyltransferase; Transferase.
SEQUENCE 384 AA; 43650 MW; 7CAA6ADC90F40032 CRC64;
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., García A.M., Gay L.J., Hulyk S.W., Villanton D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrígues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeeley R.W., Touchman J.W., Green E.D., Dickson M.C., Krzywinski M.I., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Salaksa U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;
 'Generation and initial analysis of more than 15,000 full-length human
 0; Gaps
 6 WDPAGYLLYCPCMGRFGNQADHFLGSLAFAKLLNRTLAVPPWIEYQHHKPPFTNLH 61
 Gaps
 6 WDPAGYLLYCPCMGRFGNQADHFLGSLAFAKLLNRTLAVPPWIEYQHHKPPFTNLH 61
 21 WDSSGYILYCPCMGRFGNQADHFLGSLAFAKNVNRTLVVPPWIVYNHHRPPYTNVH 76
 Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Eutaryota, Neopeerygli, Taleostel, Euteleostel, Neoteleostel,
Acanthomorpha, Acanthopterygli, Percomorpha, Tetraodontiformes,
Tetradontoidea, Tetraodontidae, Takifugu.
 .
 Length 384;
 Length 380
 80.5%; Score 284; DB 2; Length 38
83.9%; Pred. No. 2.4e-27;
tive 5; Mismatches 4; Indels
 4; Indels
 Klein S., Gerhard D.S.;
Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC08219; AAH82519.1; -.
Hypothetical protein.
SEQUENCE 380 AA; 43570 MW; 8BB938CE776D5238 CRC64;
 Last sequence update)
Last annotation update)
 and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 05-JUL-2004 (TrEMBLrel. 27, Created)
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05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 80.5%; Score 284; DB 2;
80.4%; Pred. No. 2.4e-27;
iive 7; Mismatches 4;
 387 AA.
 384 AA
 Created)
 PRT;
 PRT;
 Protein-O-fucosyltransferase
 28,
28,
28,
 Query Match
Best Local Similarity 80.3.
Best Local 45; Conservative
 Local Similarity 83.9
les 47; Conservative
 PRELIMINARY;
 PRELIMINARY;
 (TrEMBLrel.
 (TrEMBLrel.
 SEQUENCE FROM N.A. TISSUE=Embryo;
 SEQUENCE FROM N.A.
 Q6EV65
Q6EV65;
25-OCT-2004 (
25-OCT-2004 (
25-OCT-2004 (
 Name=fut12;
 Query Match
 070AG7;
 Q70AG7
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Matches
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 RESULT 14
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DB Proctein-O-fucosyltransferase 1.

ON Name=fut12;

Name=fut12;

Name=fut12;

Netradon nigroviridis (Green puffer).

Extradodn nigroviridis (Green puffer).

C Eutradonon nigroviridis (Green puffer).

C Eutradonotopha; Metazoa; Chordata; Euteleostei; Neoteleostei;

OC Actinopterygii; Neopterygii; Percomorpha; Tetraodontiformes;

OC Tetradonotoldea; Tetraodontidae; Tetraodon.

OX NCBI TAXID=9983;

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RN NI TAXID=9983;

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|------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------|----------------------------------------------|-------------------------------------------------------------------------------------|---------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| GenCore version 5.1.6<br>Copyright (c) 1993 - 2005 Compugen Ltd. | OM protein - nucleic search, using frame_plus_p2n model Run on: October 26, 2005, 05:08:04; Search time 1382.21 Seconds (without alignments) 2138.440 Million cell updates/sec | Title: US-09-774-954-9 Perfect score: 353 Sequence: 1 MPAGSWDPAGYLLYCPCMGRLAVPPWIEYQHHKPPFTNLH 61 | Scoring table: BLOSUW62 Kgapop 10.0 , Kgapext 0.5 Ygapop 10.0 , Ygapext 0.5 Ygapop 6.0 , Fgapext 7.0 Delop 6.0 , Delext 7.0 | Searched: 4708233 segs, 24227607955 residues | Total number of hits satisfying chosen parameters: 9416466 Minimum DB seq length: 0 | sey rength:<br>ssing: Minim<br>Maxim<br>Listi           | Command line parameters: -MODEL=frame+ p2n.model -DEV=x1h -Q=/cgn2_1/USFTO_spool_h/US09774954/runat_25102005_105432_6389/app_query.fasta_1.917 -Q=/cgn2_1/USFTO_spool_h/US09774954/runat_25102005_105432_6389/app_query.fasta_1.917 -DB=GenEmbl -QFWT=fastap -SUFPIX=rege -MINMATCH=0.1 -LOOPCI_=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE.pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFWT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -USER=US09774954_GCGN 1 1 4966_GCNTat_2102005_105432_6389 -NCPU=6 -ICPU=3 -NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSDELOCK=100 -LONGLOG -LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -KGAPOP=10 -KGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7 | Database : GenEmbl:*  1: gb_ba:* 2: gb_htg:* 3: gb_on:* 4: gb_on:* 5: gb_ov:* 6: gb_pat:* 7: gb_ph:* 10: gb_ph:* 11: gb_ets:* 11: gb_ets:* 12: gb_et:* 14: gb_vi:* | Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. | SUMMARIES Result Query No. Score Match Length DB ID Description | 1 353 100.0 1100 6 ARL63457 ARL63457 Sequence<br>2 353 100.0 1100 6 BD103196 BD103196 O-fucosyl<br>3 353 100.0 1167 6 CQ727777 CQ727777 Sequence<br>4 353 100.0 1167 9 AJ781500 AJ781500 Pan trogl |

| AR163452 Sequence BD103189 O-fucosy1 AR163451 Sequence BD103189 O-fucosy1 BC000582 Homo sapin AC0022 Homo sapin AC0022 Homo sapin BE000284 Homo sapin AR375884 Homo sapin AX344580 Bos tauru AX344580 Bos tauru AX344580 Bos tauru AX344580 Bos tauru AX344580 Bos tauru AX344580 Bos tauru AX344580 Bos tauru AX34459 Rattus no AX3715885 Gallus ga AX375885 Gallus ga AX378150 Partus no AX381504 Tetraodon BC082519 Xenopus t AX3781498 Silurana AX314490 Drosophil AX603444 Rattus no AX181501 Mus muscu AX803572 Drosophil AR503572 Drosophil AR503572 Drosophil AR164453 Sequence BD103191 O-fucosy1 AX112708 Ciona int                                                                                                                                                                                                                                                                                                                                                                                                          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| 5         353         100.0         1300         6         AR163452           7         353         100.0         1514         6         BD103188           9         353         100.0         1514         6         BD103188           10         353         100.0         1514         6         BD103188           11         353         100.0         1524         9         BC000582           11         353         100.0         5269         9         HSM803330           12         353         100.0         5266         6         AX780153           13         353         100.0         5269         9         AK780153           15         343         90.0         5189         9         DB0002           16         343         90.0         5189         9         DB0002           17         341         96.6         1176         4         AX344581           16         343         90.0         1134         4         SSC567917           20         32         190.0         1134         4         AX344581           21         30         87.3         1152 <td< td=""><td>AR163457 ON Sequence 16 from Sequence 16 from Sequence 16 from AR163457.1 GI: i Unknown. SM Unknown. SM Unknown. i Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. 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Unclassified.</td><td>s: 355.00<br/>snt Similarity: 100.00<b>%</b><br/>Local Similarity: 100.00<b>%</b><br/>/ Match: 6</td></td<> | AR163457 ON Sequence 16 from Sequence 16 from Sequence 16 from AR163457.1 GI: i Unknown. SM Unknown. SM Unknown. i Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. Unclassified. 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| 7                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      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AJ781500 1167 bp mRNA linear PRI 07-JUL-2004
Pan troglodytes mRNA for protein-O-fucosyltransferase 1 (fut12
 129
 linear PAT 03-FEB-2004
 Venter,C.J., Adams,M.C., Li,P.W. and Myers,B.W.
Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
121 ACCTIGGCIGICCCICCTIGGAIIGAGIACCAGCAICACAAGCCICCTIICACCAACCIC 180
 9948-8.
AJ781500.
AJ781500.
AJ781500.1 GI:50057069
Fut12 gene; pofut1 gene; protein-O-fucosyltransferase 1.
Pan troglodyres (chimpanzee)
Pan troglodyres
Elexaryota; Metazoa (Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
 Martinez-Duncker,I., Mollicone,R., Candelier,J.J., Breton,C. and Oriol,R.
A new superfamily of protein-O-fucosyltransferases,
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61
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 thereof
Patent: WO 02068579-A 13711 06-SEP-2002;
PE Corporation (NY) (US)
Location/Qualifiers
1. 116.7
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
 Length:
Matches:
Conservative:
Mismatches:
Indels:
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Sequence 13711 from Patent W002068579.
CQ727777. GI:42294771
 Gaps:
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 1.19e-35
353.00
100.00%
100.00%
 Homo sapiens (human)
Homo sapiens
 Percent Similarity:
Best Local Similarity: 1
Query Match:
 250 CAT 252
 181 CAT 183
 61 His 61
 61 His 61
 Alignment Scores:
 ACCESSION
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 PAT 27-AUG-2002
 ThrieualavalproprofrpileGluTyrGlnHisHisLysProproPheThrAsnLeu 60
 08/978741 PI
 Unidentified
Up 2001527389-A/9
JP 2001527389-A/9
17-DEC-1997 UP 1998532877
31-DAN-1997 US 08/792498,26-NOV-1997 US NG WANG, MICHAEL W SPELLMAN
C12N15/54,C12N9/10,C07K16/40
Strandedness: Single;
Topology: Linear;
O-fucosyltransferase
 linear
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 Length:
Matches:
Conservative:
Mismatches:
Indels:
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 US-09-774-954-9 (1-61) x BD103196 (1-1100)
 US-09-774-954-9 (1-61) x AR163457 (1-1100)
 1.12e-35
353.00
100.00%
100.00%
 Percent Similarity:
Best Local Similarity:
Query Match:
DB:
 181 CAT 183
 61 His 61
 BD103196
 Alignment Scores:
Pred. No.:
 41
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ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
 REFERENCE
AUTHORS
TITLE
JOURNAL
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BD103196
LOCUS
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Percent Similarity:
Best Local Similarity:
Query Match:
 316 CAT 318
 His 61
 Alignment Scores:
Pred. No.:
 Alignment Scores:
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 61
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DEFINITION
ACCESSION
VERSION
KEYWORDS
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 Pred. No.:
REFERENCE
AUTHORS
TITLE
JOURNAL
 RESULT 6
BD103189
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Neuherberg, GERMANY
Clone from S. Witemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing
consortium of the German Genome Project.
This clone (DKFZ9451J114) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
information about the clone and the sequencing project is available
at http://mips.gsf.de/proj/cDNA/.
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 Galthersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov/
Shther,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
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Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
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Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
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Young,A., Zhang,L.-H. and Green,B.D.
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Series: IRAL Plate: 5 Row: o Column: 9
This clone was selected for full length sequencing because it
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Submitted (15-NOV-2000) National Institutes of Health, Mammalian
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 'product="protein O-fucosyltransferase 1, isoform 2
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On Oct 8, 2003 this sequence version replaced gi:12653608.
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
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Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
 human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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 Nagase, T., Seki, N., Ishikawa, K., Tanaka, A. and Nomura, N. Prediction of the coding sequences of unidentified human genes. V. The coding sequences of 40 new genes (KIAA0161-KIAA0200) deduced by analysis of cDNA clones from human cell line KG-1 DNA Res. 3 (1), 17-24 (1996)
 linear PRI 10-JAN-2003
 170
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 21 PheGlyAsnGlnAlaAspHisPheLeuGlySerLeuAlaPheAlaLysLeuLeuAsnArg 40
 Homo sapiens (human)
Homo sapiens sapiens sapiens
Ebkaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Chiang, P.W., Wang, S., Smithivas, P., Song, W.J., Ramamoorthy, S., Hillman, J., Puett, S., Van Keuren, M.L., Crombez, E., Kumar, A., Glover, T.W., Miller, D.E., Tash, C.H., Blackburn, C.C., Chen, X.N., Sun, Z., Cheng, J.F., Korenberg, J.R. and Kurnit, D.M. Identification and analysis of the human and murine putative chromatin structure regulator SUPPTGH and Supt6h 96374824
 1 MetProAlaGlySerTrpAspProAlaGlyTyrLeuLeuTyrCysProCysMetGlyArg
 4560
61
0
0
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 Length:
Matches:
Conservative:
Mismatches:
Indels:
 5189 bp mRNA
Homo sapiens KIAA0180 mRNA, complete cds.
D80002. GI:20521837
 Gaps:
 US-09-774-954-9 (1-61) x HSM803330 (1-4560)
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100.00%
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 Percent Similarity:
Best Local Similarity:
 231 CAT 233
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1 (bases 1 to 5249)
Mang,Y., Sho,L., Shi,S., Harris,R.J., Spellman,M.W., Stanley,P. and Haltiwanger,R.S.
Modification of epidermal growth factor-like repeats with O-fucose. Molecular cloning and expression of a novel GDP-fucose protein O-fucosyltraniserase

O-fucosyltraniserase

21523965
11524432
 AF375884 153-OCT-2001 S249 bp mRNA linear PRI 23-OCT-2001 Homo sapiens protein o-fucosyltransferase (POFUT1) mRNA, complete
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Wang, Y. and Spellman, M.W.
 BD103190.1 GI:22648764
JP 2001527389-A/3.
 5.94e-35
353.00
100.00%
100.00%
 O-fucosyltransferase.
 GENENTECH INC
OS Unidentif
OS Unidentif
OS JD 25-DEC-19
PR 31-JAN-19
YANG WANG, MICH
PC C12N15/54
CC TCD01099:
CC TCD01099:
FT ROWYCE
FT ROWICE
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 Percent Similarity:
Best Local Similarity:
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 61 His 61
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 Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Direct Submission
Submitted (02-MAY-2001) Cell Biology, Albert Einstein College of
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Location/Qualifiers
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Shi,S., Stanley,P., Wang,Y., Shao,L., Harris,R.J., Spellman,M.W.
and Haltiwanger,R.S.
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PAT 27-AUG-2002
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 1 MetProAlaGlySerTrpAspProAlaGlyTyrLeuLeuTyrCysProCysMetGlyArg
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Haferlach, T., Schoch, C., Kern, W., Kohlmann, A., Schnittger, S. Dugas, M., Eils, R., Brors, B. and Mergenthaler, S. Novel genetic markers for leukemias Patent: WO 3033443-A 2310 15-MAY-2003; Deutsches Krebsforschungszentrum (DE); Ludwig-maximilian-Universiteet Muenchen (DE); Haferlach, To: PD Dr. (DE); Schoch, Claudia (DE); Kern, Wolfgang (DE) Dr. Location/Qualifiers
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31-JAN-1997 US
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259 CAT 261
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 41 ThrieualaValProProTrpileGluTyrGlnHisHisLysProProPheThrAsnLeu 60
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Bos taurus protein O-fucosyltransferase 1b (pofut1) mRNA, complete
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 Direct Submission
Submitted (17-JUL-2003) EA 3176 Glycobiologie et Biotechnologie,
Faculte des Sciences et Techniques, 123, Avenue A. Thomas, Limoges
87060, France
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BI524031 603052202 BF315757 601900828 BU155142 AGENCOURT C0774833 ILLUMIGEN BI199190 602788739 BE260030 60150556

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CF155036 BB618795

BY728018

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BM478111

BB633858

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This is the 5' sequence of the clone insert Clone from S. Wiemann,
Molecular Genome Analysis, German Cancer Research Center (DKFZ);
Email s.wiemann@dkfz-heidelberg.de; sequenced by BMFZ (Biomedical
Research Center at the Heinrich-Heine-University,
Duesseldorf/Germany) within the cDMA sequencing consortium of the
German Genome Project. This clone (DKFZp459B068) is available at
the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum,
Heubnerweg 6, 14059 Berlin-Charlottenburg, GERWANY; Email:
clone@rzbd.de Further information about the clone and the
sequencing project is available at
http://mips.gsf.de/projects/cdma/.
 Pongo pygmaeus
Wakaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Pongo.
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 Koehrer, K., Beyer, A., Mewes, H.W., Weil, B., Amid, C., Osanger, A., Fobo, G., Han, M. and Wiemann, S. Pongo pygmaeus mRNA (Koehrer, K., Beyer, A., Mewes, H.W., et al.) Unpublished (2004)
 520 bp mRNA linear EST 07-JUL-
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 REFERENCE
AUTHORS
 TITLE
JOURNAL
COMMENT
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KEYWORDS
SOURCE
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-DEVALIGN=200 -LOOPEXT=0
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CN348925 170005328
 October 26, 2005, 05:59:38 ; Search time 1065.43 Seconds (without alignments) 2179.320 Million cell updates/sec
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 Description
 1 MPAGSWDPAGYLLYCPCMGR.....LAVPPWIEYQHHKPPFTNLH
 68479088
 GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
 - nucleic search, using frame_plus_p2n model
 34239544 segs, 19032134700 residues
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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 Sequence:
 Searched:
 Database
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Result No.

EST 07-JUL-2004

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BB642654 BY728337 B

us-09-774-954-9.rst

Alignment

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Mismatches:
Indels:
Gaps:
 Length:
Matches:
 High quality sequence stop: 551.
Location/Qualifiers
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 CN348927 550 bp mRNA linear EST 16-MAY-2004
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1 (bases 1 to 550)
Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J., Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R., Lebkowski, J and Stanton, L.W.
Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation
Nat. Biotechnol. 22 (6), 707-716 (2004)
Regenerative Medicine
 40
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 41 ThrLeuAlaValProProTrplleGluTyrGlnHisHisLysProProPheThrAsnLeu
 230 Constitution Drive, Menlo Park, CA 94025, USA Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
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Conservative:
Mismatches:
Indels:
 Gaps:
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 CN348927
CN348927.1 GI:47348861
 1.52e-33
353.00
100.00%
100.00%
 Homo sapiens (human)
Homo sapiens
 Geron Corporation
 Percent Similarity:
Best Local Similarity:
 296 CAT 298
 61 His 61
 Scores:
 EST.
 Best Local S:
Query Match:
 LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
 . No.:
 JOURNAL
COMMENT
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RESULT 2 CN348927

REFERENCE AUTHORS

TITLE

FEATURES

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//mol type="mRNA"
//mol type="mRNA"
//mol type="mRNA"
//mol type="mencoblastoma"
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//clone="IMAGE:1508464"
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Note: this is a NIH_MGC Library."
 EST.

Homo sapiens (human)

Homo sapiens

Homo sapiens

Homo sapiens

Homo sapiens

Extrayora; Netzeara; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

EST.

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-romail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Libla at: image.llnl.gov

Hish Account of the I.M.A.G.E. Consortium/Libla at: image.llnl.gov
 551 bp mRNA linear EST 26-OCT-2000 GO152208F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3508464 5', BE26136
conditions. Embryoid bodies were generated in the presence of all-trans retinoic and mitogens."
 228
 21 PheGlyAsnGlnAlaAspHisPheLeuGlySerLeuAlaPheAlaLysLeuLeuAsnArg 40
 169 TTTGGGAACCAGGCGGATCACTTCTTGGGCTCTCTGGCATTTGCAAAGCTGCTAAACCGT
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1.73e-33
353.00
100.00%
100.00%
 1.8e-33
353.00
100.00%
100.00%
 Homo sapiens (human)
 Homo sapiens
 Score:
Percent Similarity:
Best Local Similarity:
 Percent Similarity:
Best Local Similarity:
 334 CAT 336
 61 His 61
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ACCESSION
VERSION
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SOURCE
ORGANISM
 Pred. No.:
 REFERENCE
AUTHORS
 RESULT 5
CN348926
LOCUS
 JOURNAL
 FEATURES
 TITLE
 COMMENT
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 Score:
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 à
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/lab_host="HHIOB (phage-resistant)"
/lab_host="HHIOB (phage-resistant)"
/clone_lib="NIH_MGC_19"
/clone_lib="NIH_MGC_19"
/note="Organ: brain; Vector: pOTB7; Site_1: XhoI; Site_2:
BCORI; CDNA made by oligo-dT priming. Directionally
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adaptor: GGCAKCGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California. Berkeley) using 2AP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
 BE262956 576 bp mRNA linear EST 26-OCT-2000 601147417F1 NIH MGC_19 Homo sapiens cDNA clone IMAGE:3162533 5', mRNA sequence.
BE262956
 219
 40
 Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 576)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
 cDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution information can be found through the I.M.A.G.E. Consortium/LiNL at: image.llnl.gov Plate: LiCMA122 row: b column: 06 High quality sequence start: 11 High quality sequence start: 11 High quality sequence.
 21 PheGlyAsnGlnAlaAspHisPheLeuGlySerLeuAlaPheAlaLysLeuLeuAsnArg
 160 TTTGGGAACCAGGCCGATCACTTTGTTTTGCAAAGCTGCTAAACGT
 551
61
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0
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Matches:
Conservative:
Mismatches:
Indels:
 1. 576
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3162533"
 Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
 Gaps:
 US-09-774-954-9 (1-61) x BE261136 (1-551)
 Location/Qualifiers
 BE262956.1 GI:9136425
 1.64e-33
353.00
100.00%
100.00%
 EST.
Homo sapiens (human)
 Percent Similarity:
Best Local Similarity:
Query Match:
 280 CAT 282
 61 His 61
 Alignment Scores:
Pred. No.:
 ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
 RESULT 4
BE262956
LOCUS
DEFINITION
 REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
 FEATURES
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ORIGIN
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="embryonic stem cells, cell lines H1, H7, and
 EST 16-MAY-2004
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/note="oligo dT_primed, full-length enriched cDNA library
from undifferentiated hBS cell lines H1 (p32), H7 (p29),
and H9 (p26) maintained in feeder-free conditions"
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 595)

1 (bases 1 to 595)

1 (bases 1 to 595)

1 (bases 2 to 595)

1 (based 2 to 596)

1 (based 3 to 596)

1 (based 3 to 596)

1 (based 3 to 596)

1 (based 3 to 596)

1 (based 3 to 596)

1 (based 3 to 596)

1 (based 3 to 596)

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1 (based 3 to 596)

1 (based 3 to 596)

1 (based 3 to 596)

1 (based 3 to 596)

1 (based 3 to 596)

2 (control human ES cell growth and differentiation at 596)

Nat. Biotechnol. 22 (d), 707-716 (2004)

Regenerative Medicine
 213
 273
 40
 1 MetProAlaGlySerTrpAspProAlaGlyTyrLeuLeuTyrCysProCysMetGlyArg
 21 PheGlyAsnGlnAlaAspHisPheLeuGlySerLeuAlaPheAlaLysLeuLeuAsnArg
 LN348926
17000532646873 GRN_ES Homo sapiens CDNA 5', mRNA sequence.
CN348926
 Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 595 Std Error: 0.00.
 595
61
0
0
0
576
61
0
0
0
 Conservative:
Mismatches:
Indels:
iength:
Matches:
Conservative:
Mismatches:
Indels:
 Length:
Matches:
 (1-576)
 CN348926.1 GI:47348860
 US-09-774-954-9 (1-61) x BE262956
 Query Match:
DB:
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CV029252
CV029252.1 GI:51487402
 Homo sapiens (human)
Homo sapiens
 293 CAT 295
 61 His 61
 VERSION
KEYWORDS
SOURCE
ORGANISM
 LOCUS
DEFINITION
 REFERENCE
AUTHORS
 TITLE
JOURNAL
COMMENT
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 RESULT 7
CV029252
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 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E 11, M.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

L Unpublished (2001)

On Feb 15, 2001 this sequence version replaced gi:31277525.

Contact: Genoscope - Centre National de Sequencage

Contact: Genoscope - Centre National de Sequencage

2 rue Gaston Cremiaux, CP 5706 - 91057 EVRX cedex - FRANCE

Email: segref@genoscope.ons.fr. Web: www.genoscope.cns.fr

1st strand cDNA was primed with a NorI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Nor I and cloned into the Nor I and EcoR V sites of the pCWNSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
 ALS55719 610 bp mRNA linear EST 30-MAR-2004 ALS55719 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens CDNA clone CSODK003YN13 5-PRIME, mRNA sequence.
ALS55719 ALS55719.3 GI:45860448
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/db xref="letaxon:9606"
/clone="CSORGO3YN13"
/cell_type="HELA CELLS COT 25-NORWALIZED"
/cell_type="HELA CELLS COT 25-NORWALIZED"
/coll_the="HELA"
/coll_type="The grand of DNA was primed with a Not1-oligo(dT)
primer. Five prime and enriched, double-strand cDNA was
digested wich Not I and cloned into the Not I and ScoR V
dites of the pCMVSPORT 6 vector. Library was normalized."
 218
 21 PheGlyAsnGlnAlaAspHisPheLeuGlySerLeuAlaPheAlaLysLeuLeuAsnArg 40
 For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSODK003CG07QP1&c=9980.f. Location/Qualifiers
 610
61
0
 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
US-09-774-954-9 (1-61) x CN348926 (1-595)
 1.85e-33
353.00
100.00%
100.00%
 Homo sapiens (human)
 Homo sapiens
 279 CAT 281
 61 His 61
 Alignment Scores:
Pred. No.:
Score:
 LOCUS
 ORGANISM
 ACCESSION
VERSION
KEYWORDS
SOURCE
 REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
 RESULT 6
AL555719
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(1-610)

US-09-774-954-9 (1-61) x AL555719

Percent Similarity: Best Local Similarity: Query Match: DB:

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/note="Vector: mixed, The ORFs were PCR amplified from the MGC (Mammalian Gene Collection) as of April 2004 and cloned by recombinational Gateway cloning into pDONR233 Donor vector. Reference: MGC (Mammalian Gene Collection) Program Team, Generation and Initial Analysis of more than 15,000 Pull-inength Human and Mouse cDNA Sequences. PNAS, 2002, 99(26), 16899-16903"
 CV029252 656 bp mRNA linear EST 20-AUG-2004 7968 Full Length cDNA from the Mammalian Gene Collection Homo sapiens cDNA 5' similar to BC000582, mRNA sequence.
 Genome Res. (2004) In press
Genome Res. (2004) In press
Marc Vidal Laboratory
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 5180
Fax: 617 632 5139
Fax: 617 632 5139
Faxis barc Vidal@dfci.harvard.edu
ORP Sequence Tag (OST) of Gateway Entry construct. Each cloned ORF results from a PCR reaction using an MGC full-length cDNA as
PCR PRIMERS
232
 40
 Land, J.F., Hiozane-Kishikawa, T., Hao, T., Bertin, N., Li, S., Diroct, A., Li, N., Rosenberg, J., Lamesch, P., Vidalain, D. O., Clingingsmith, T., Hartley, J.L., Esposito, D., Cheo, D., Moore, T., Simmons, P., Sequerra, R., Bosak, S., Doucette-Stamm, L., Le Peuch, C., Vandenhaute, J., Cusick, M. E., Albala, J.S., Hill, D. B. and Vidal, M. Human ORFeome Version 1.1: a Platform for Reverse Proteomics
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 656)
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Collection"
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BACKWARD: ATGGGCGCCGCGTGGGC
BACKWARD: CACCTTGGGAAGATAAGGTA
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Plate: 11019 row: 04 column: B
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 ACCESSION
VERSION
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 Pred. No.:
 DEFINITION
 REFERENCE
 AUTHORS
 JOURNAL
 RESULT 9
CN348925
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 Score:
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 HRI human cuwn profile to the contact Takkon Isogai Contact: Takkon Isogai Genomics Laboratory Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
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 190 ACCTTGGCTGTCCTCCTTGGATTGAGTACCAGCATCACAAGCCTCTTTCACCAACCTC 249
 20
 40
 9
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (bases I to 69)

Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y., Yamamotto, J., Wakamatsu, A., Nakamura, Y., Nagai, T., Sugano, S. and
 41 ThrLeuAlaValProProTrpIleGluTyrGlnHisHisLysProProPheThrAsnLeu
 1 MetProAlaGlySerTrpAspProAlaGlyTyrLeuLeuTyrCysProCysMetGlyArg
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EST. Homo sapiens (human)
Homo sapiens
 2.18e-33
353.00
100.00%
100.00%
 2.02e-33
353.00
100.00%
100.00%
 Percent Similarity:
Best Local Similarity:
Query Match:
DB:
 Percent Similarity:
Best Local Similarity:
Query Match:
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DEFINITION
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KEYWORDS
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/mol_type="mRNA"
/db xref="taxon:960"
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/note="Digo dT primed, full-length enriched cDNA library
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H1 (p22), H7 (p29), and H9 (p26) maintained in feeder-free
conditions."
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17000532814105 GRN_EB Homo sapiens cDNA 5', mRNA sequence.
CN348925
 251
 Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalla; Butheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 705)

1. (bases 1 to 705)

1. Enadenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J., Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R., Lebkowski, J. and Stanton, L. W.
 21 PheGlyAsnGlnAlaAspHisPheLeuGlySerLeuAlaPheAlaLysLeuLeuAsnArg 40
 191
 40
 20
 Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation Nat. Biotechnol. 22 (6), 707-716 (2004) Contact: Brandenberger R
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Fax: 6 rbrandenberger@geron.com
Insert Length: 705 Std Error: 0.00.
Location/Qualifiers
 705
61
0
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 Conservative:
Mismatches:
Indels:
 Length:
Matches:
 US-09-774-954-9 (1-61) x CN348925 (1-705)
 CN348925.1 GI:47348859
 Regenerative Medicine
 2.21e-33
353.00
100.00%
100.00%
 Homo sapiens (human)
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61
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0
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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EST.
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100.00%
100.00%
 Homo sapiens (human)
Homo sapiens
 Percent Similarity:
Best Local Similarity:
 301 CAT 303
 61 His 61
 Alignment Scores:
Pred. No.:
 Query Match:
DB:
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KEYWORDS
SOURCE
ORGANISM
 DEFINITION
 REFERENCE
AUTHORS
TITLE
JOURNAL
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/lab host="nBH10B (phage-resistant)"
/clone lib="NIH MGC_14"
/note="Grgan: Kidney, Vector: pOTB7; Site_1: XhoI; Site_2: BcoR1; cDNA made by oligo-dT priming. Directionally cloned into EcoR1/XhoI sites using the following 5; adaptor: GGCAGCAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
 BG424731 11H_MGC_14 Homo sapiens cDNA clone IMAGE:4591867 5', mRNA sequence.
 41 ThrLeualaValProProTrpIleGluTyrGlnHisHisLysProProPheThrAsnLeu 60
 110 TTTGGBAACCAGGCCGATCACTTCTTGGGCTCTCTGGCATTTGCAAAGCTGCTAAACCGT 169
 40
 21 PheGlyAsnGlnAlaAspHisPheLeuGlySerLeuAlaPheAlaLysLeuLeuAsnArg
 1 MetProAlaGlySerTrpAspProAlaGlyTyrLeuLeuTyrCysProCysMetGlyArg
 Length:
Matches:
Conservative:
Mismatches:
 Gaps:
 US-09-774-954-9 (1-61) x BG424731 (1-753)
 BG424731
BG424731.1 GI:13331237
 Homo sapiens (human)
Homo sapiens
 353.00
100.00%
100.00%
100.00%
 Percent Similarity:
Best Local Similarity:
 230 CAT 232
 61 His 61
 Alignment Scores:
 Best Local Sir
Query Match:
DB:
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 RESULT 10
BG424731
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AUTHORS
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JOURNAL
COMMENT
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/organism="Homo sapiens"
//organism="Homo sapiens"
//organism="mkNR"
//db xref="taxon:9606"
/clone="INAGE:3503461"
//lab host="heriol solde"
/lab host="DHIOB (phage resistant)"
/clone lib="NHH MGC 19"
/note="Corgan: brain; Vector: pOTB7; Site_1: XhoI; Site_2: RocR1; cDNA made by oligo-dr priming. Directionally cloned into EcoRI/XhoI sites using the following 5; adaptor: GGACGAG(0). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butharia; Primates; Catarrhini; Hominidae; Homo.

Mammalia; Butharia; Primates; Catarrhini; Hominidae; Homo.

Mational Institutes of Health, Mammalian Gene Collection (MGC)

Mational Institutes of Health, Mammalian Gene Collection (MGC)

LONDAubished (1999)

Contact: Robert Strausberg, Ph.D.

Email: Capbs-r@mail.nih.gov

Tissue Procurement: Arc.

CONA Library Preparation: Ling Hong/Rubin Laboratory

CONA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

NAN Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: image.llnl.gov

Plate: LLCANY6 cove o column: 14

High quality Sequence stop: 710.
 602578756F1 NIH_MGC_19 Homo sapiens CDNA clone IMAGE:3503461 5', mRNA sequence.
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Genoscope - Centrer National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
 BX345989

BX45989 Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED Homo sapiens CDNA clone CSODJ008YF12 5-PRIME, mRNA sequence.
 229 ACCTIGGCTGTCCCTCGTTGGATTGAGTACCAGCATCACAAGCCTCCTTTCACCAACCTC 288
 109 Ardccraccaccracrassaccassacrassacracracracracracracracracracarassaca 168
 169 irifdegaaccadaccartcacrictifgegcicricigecarrigcaaagcigcraaaccdi 228
 /cell type="T CELLS" (JURKAT CELL LINE) COT 10-NORMALIZED" /cell line="JURKAT" /clone lib="Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED"
202 ACCTTGGCTGTCCCTCCTTGGATTGAGTACCAGCATCACAAGCCTCCTTTCACCAACCTC 261
 ThrLeuAlaValProProTrp11eGluTyrGlnHisHisEysProProPheThrAsnLeu 60
 Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 841)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)

On May 5, 2003 this sequence version replaced gi:30377055.

Contact: Genoscope
 /note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized.
 1 MetProAlaGlySerTrpAspProAlaGlyTyrLeuLeuTyrCysProCysMetGlyArg
 21 PheGlyAsnGlnAlaAspHisPheLeuGlySerLeuAlaPheAlaLysLeuLeuAsnArg
 For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSOAJ008DC06QPl&c=9980.f. Location/Qualifiers
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61
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0
0
 Length:
Matches:
Conservative:
Mismatches:
Indels:
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/db_xref="taxon:9606"
/clone="CS0DJ008YF12"
 US-09-774-954-9 (1-61) x BX345989 (1-841)
 BX345989.2 GI:46549776
 353.00
100.00%
100.00%
100.00%
 2.73e-33
 Homo sapiens (human)
 j. .841
 Percent Similarity:
Best Local Similarity:
Query Match:
 262 CAT 264
 61 His 61
 BX345989
 Alignment Scores:
 41
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BX345989
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 /organism="Homo sapiens"
/mol_type="mRNA"
/db_zref="taxon:9606"
/db_zref="taxon:9606"
/clone="TMAGE:4842061"
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/Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library. |
 BG747760 808 bp mRNA linear EST 15-MAY-2001
602705255F1 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:4842061 5',
 40
 41 ThrLeuAlaValProProTrpIleGluTyrGlnHisHisLysProProPheThrAsnLeu 60
 Homo sapiens
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to, 808)
 .09
 1 MetProAlaGlySerTrpAspProAlaGlyTyrLeuLeuTyrCysProCysMetGlyArg
 21 PheGlyAsnGlnAlaAspHisPheLeuGlySerLeuAlaPheAlaLysLeuLeuAsnArg
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1675 row: n column: 14
High quality sequence stop: 808.
 NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
 808
61
0
0
 Length:
Matches:
Conservative:
Mismatches:
Indels:
 Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
 Gaps:
 US-09-774-954-9 (1-61) x BG747760 (1-808)
 BG747760.1 GI:14058413
 353.00
100.00%
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 Homo sapiens (human)
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 mRNA sequence.
 Percent Similarity:
Best Local Similarity:
 300 CAT 302
 61 His 61
 Alignment Scores:
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E l'basez l'ordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E l'bases l'os 898.

E NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L'Ompublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin information can be found through the I.M.A.G.E. Consortium/LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov

High quality sequence stop: 721.
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//organism="Homo sapiens"
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//lab_host="DHIOB (phage=resistant)"
//clone lib="NIH MGC 19"
//note="Organ: brain, Vector: pOTB7; Site 1: XhoI; Site_2:
//note="Organ: brain, Vector: poTB7; Site 1: XhoI; Site_2:
//note="Organ: brain, Vector: poTB7; Site_1: XhoI; Site_2:
//clone into EcoRI/XhoI site using the following 5/
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
 BF315757 898 bp mRNA linear EST 21-NOV-2000 601900828F1 NIH_MGC_19 Homo sapiens CDNA clone IMAGE:4129975 5',
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 1 MetProAlaGlySerTrpAspProAlaGlyTyrLeuLeuTyrCysProCysMetGlyArg
 180 Tringgaaccaggccgarcacrrcriggcrrcrcrgcarrrgcaaagcrgcraaaccgr
 898
61
0
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 Length:
Matches:
Conservative:
Mismatches:
Indels:
 Gaps:
 US-09-774-954-9 (1-61) x BF315757 (1-898)
 mRNA sequence. _ _ BF315757.1 GI:11264027
 Homo sapiens (human)
Homo sapiens
 353.00
100.00%
100.00%
 Percent Similarity:
Best Local Similarity:
 267 CAT 269
 61
 61 His
 Alignment Scores:
 Query Match:
DB:
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 BF315757
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 /organism="Homo sapiens"
//organism="Homo sapiens"
//organism="MAGE:201616"
//lone="INAGE:201616"
//lone="INAGE:201616"
//lone="Organ: pooled lung and spleen; Vector: pcMV-SPORT6;
Site 1: Not1; Site 2: BcoW (destroyed); RNA source
anonymous pool of 24 week female lung, 16 week female
spleen, and 20-22 week male spleens. Library is oligo-dr
primed and directionally cloned (Brook site is destroyed
upon cloning). Average insert size 1.4 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 026. Note:
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.

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 BIS24031 889 bp mRNA linear EST 29-AUG-2001 603052202F1 NIH_MGC_122 Homo sapiens CDNA clone IMAGE:5201616 5', mRNA sequence.
BIS24031 GI:15348823
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 40
 21 PheGlyAsnGlnAlaAspHisPheLeuGlySerLeuAlaPheAlaLysLeuLeuAsnArg
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61
0
0
0
 Length:
Matches:
Conservative:
Mismatches:
Indels:
 US-09-774-954-9 (1-61) x BI524031 (1-889)
 2.92e-33
353.00
100.00$
100.00$
 Homo sapiens (human)
Homo sapiens
 Percent Similarity:
Best Local Similarity:
Query Match:
DB:
61 His 61
||||
289 CAT 291
 Alignment Scores:
Pred. No.:
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VERSION
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SOURCE
ORGANISM
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 REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
 RESULT 14
 BI524031
 FEATURES
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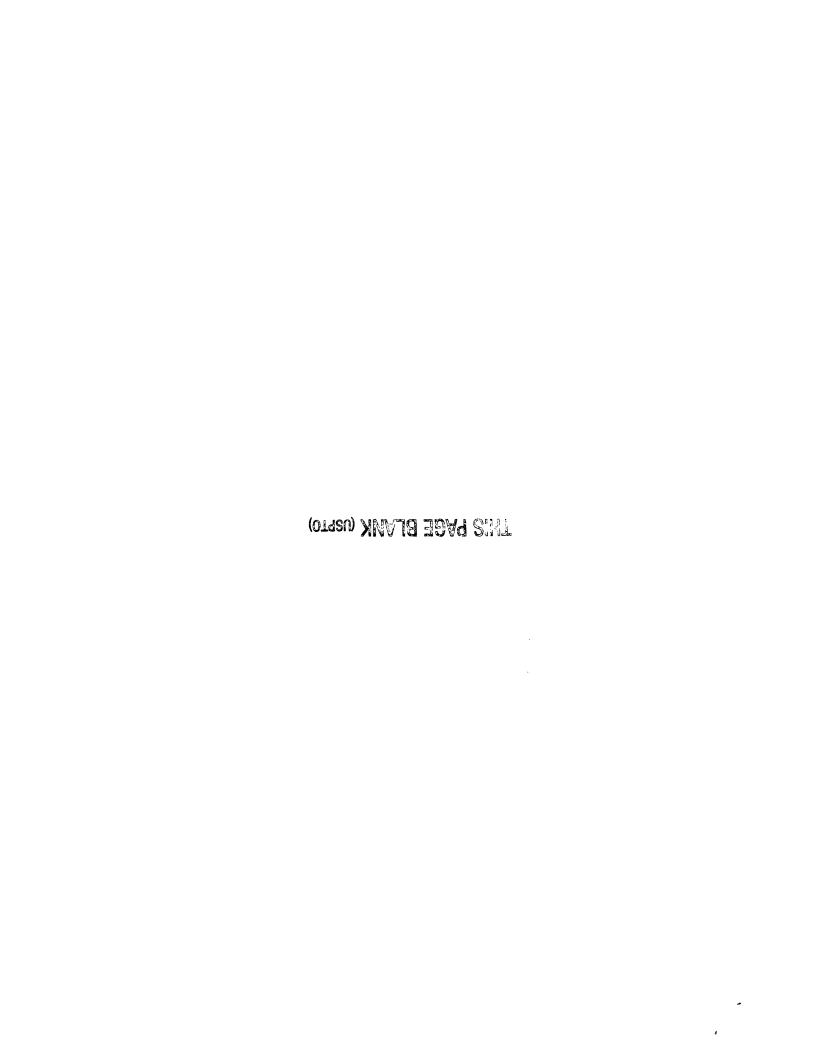
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300 CAT 302

Search completed: October 26, 2005, 15:17:27 Job time : 1069.43 secs



against INA

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Command line parameters:
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-MODEL=frame+ p2n.model -DEV=xlh
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-Q=/Cogn2 1/UGPFO bpool h/USO9774954/runat_25102005_105434_6433/app_query.fasta_1.917
-DB=Published Applications NA -OFFT=1 -END=1 -MAFRIX=blosum62
-LOOPCL=0 -LOŌPEXT=0 -UNITS=bits -START=1 -END=1 -MAFRIX=blosum62
-TRANS=humand_0 cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFWT-pct -NORM=ext -HEAPSTZE=500 -MINLEN=0
-MAXTEN=2000000000 -USER=USO9774954_@CGN 1 1 684 @runat 25102005_105434_6433
-NCPU=6 -ICPU=3 -NO MMAP -LAGREQUERY -NEG GCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DBV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
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 October 26, 2005, 09:31:14 ; Search time 260.659 Seconds (without alignments) 1931.299 Million cell updates/sec
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 1 MPAGSWDPAGYLLYCPCMGR......LAVPPWIEYQHHKPPFTNLH
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
 OM protein - nucleic search, using frame_plus_p2n model
 Total number of hits satisfying chosen parameters:
 9772377 segs, 4126317084 residues
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
 Minimum DB seq length: 0
Maximum DB seq length: 2000000000
 US-09-774-954-9
353
 BLOSUM62
 Title:
Perfect score:
 Scoring table:
 Sequence:
 Searched:
 Database
 Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

|     |                       |          | æ                 |                                                        |        |                                    |                    |
|-----|-----------------------|----------|-------------------|--------------------------------------------------------|--------|------------------------------------|--------------------|
| Res |                       | - 5      | Query<br>Match    | Length                                                 | DB     | ID                                 | Description        |
| 1   | :                     | ı ın     | . 6               | 1100                                                   | ; ¬    | -60-                               | Sequence 16, App   |
|     | 1 73                  | ഥ        | 00                | 1300                                                   |        | -09-774-954-4                      | equenc             |
|     | m                     | ம        | 00                | 1400                                                   |        | -10-956-157-9986                   | equenc             |
|     | 4                     | ı        | 00                | 1506                                                   |        | -10-956-157-475                    | equenc             |
|     | N.                    | ഗി       | 99                | 1514                                                   |        | -09-774-954-1                      | equenc             |
|     | φt                    | ∟n ∟     | 96                | 5218                                                   |        | -10-301-822-168<br>-10-056-157-475 |                    |
|     | - α                   | 3 5 5    | : -               | 11284                                                  |        | 774-954-5                          | en c               |
|     | ٥                     | $r \sim$ | 93                | 1209                                                   | 1      | -11-097-143                        | equenc             |
|     | 10,                   | -        | : -:              | 5009                                                   |        | -09-774-954-7                      | equenc             |
| υ   | 11                    | 00       | ĸ.                | 3264                                                   |        | -11-097-143-1816                   | equenc             |
| υ   | 12                    | ∞ .      | ë.                | 3793                                                   |        | -11-097-143-18082                  | edneuc             |
| υ   | 13                    | $\alpha$ | ÷.                | 521                                                    |        | 9-925-065A-602                     | equenc             |
|     | 14                    | NO       | et u              | 760                                                    |        | -IU-820-4/4A-23                    |                    |
|     | 15                    | 2 6      |                   | 165                                                    |        | 39-864-761-2644<br>39-864-761-2644 | equence            |
|     | 17                    | 8 6      |                   | 591                                                    |        | 10-029-386-248                     | Seguenc            |
|     | 18                    | 86       | •                 | 447                                                    | 21     | -425-115-1423                      | Sequenc            |
|     | 19                    | ω,       | ë.                | 402                                                    | σ;     | 783-590-11501                      | quence             |
|     | 50                    | 80.2     | 22.8              | 823                                                    | 9.5    | US-10-424-599-1232/6               | Sequence 1232/6, A |
|     | 22                    | : .      |                   | 1617                                                   | 202    | -437-963-114                       | equenc             |
| υ   | 23                    |          |                   | 277616                                                 | 20     | -367-094                           | equenc             |
|     | 24                    | ë.       | ö                 | 1803                                                   | 16     | US-10-156-761                      | equenc             |
|     | 52                    | ຕ່       | ö                 | 560                                                    | ~<br>- | 0-156-761-1                        | Sequence 1, Appli  |
| ,   | 9 5                   | 73       |                   | 3545                                                   | 9 0    | -09/-143-11<br>960-252-106         | 10634 A            |
| טנ  | , c                   | 27       | 200               | 4.3                                                    | n o    | 960-352-1656                       | 1656,              |
| טע  | 562                   | 72       |                   | 447                                                    |        | 9-960-352-66                       | 6689, Ap           |
| )   | 30                    | 71       |                   | 1186                                                   | 7      | 10-282-122A-264                    | e 26446,           |
|     | 31                    | 71       | ö                 | 1242                                                   | -      | 10-282-122A-2817                   | e 28170,           |
| υ   | 32                    | ۳,       | · •               | 4953                                                   | α,     | 10-437-963-2396                    | S 23967,           |
|     | 33                    | •        | · .               | 467                                                    | ٠,     | 70-778-876-60<br>7001 701 010 01   | 10060              |
| UI  | ى د<br>4 ت            | ີ່.      | ٠.                | 010                                                    | ٦ ،    | 10-029-366-1006                    | e 56. App          |
| ט כ | n 49                  | 69.5     | . 6               | í                                                      |        | 10-437-963-1559                    | e 15591,           |
| ט   | 37                    | , Ψ      | . 6               | 9                                                      | 7      | 10-972-079-3289                    | e 32895,           |
| U   | 38                    | æ        | ę.                | 909                                                    | Ò      | 0-972-079-4387                     | e 43878,           |
| υ   | 39                    | œ.       | φ.                | 009                                                    | Ċ (    | -10-972-079-                       | e 43879,           |
| υ   | 40                    | œ (      | 4.6               | 600                                                    |        | 72-079-4388                        | e 45000,           |
|     | 4 4                   | ρo       | 7.0               | 53/3                                                   | - 0    | 5-10-103-963-<br>-09-863-475A-     | 5. Appli           |
| C   | 7 7                   | o r      | 'nσ               | 47.5                                                   |        | S-10-425-115-5044                  | Sequence 50448,    |
| J   | 7 7                   | ٠,       | 10.1              | 909                                                    | Ñ      | S-10-972-079-                      | e 27372,           |
| υ   | 45                    | 67.5     | 0                 | 636                                                    |        | S-09-925-065A-285                  | equence 2857       |
|     |                       |          |                   |                                                        |        | ALIGNMENTS                         |                    |
| RES | SULT 1                |          |                   |                                                        |        |                                    |                    |
| is` | -09-774               | 74-954-1 | 16                | 1000                                                   | 9      | 1                                  |                    |
|     | Sequence<br>Publicati | cation N | Appile<br>No. US2 | uence 16, Application US/<br>lication No. US2004024164 | 25     | 7                                  |                    |
|     | GENE                  | ERAL INE | PORMATI           | ON:                                                    |        |                                    |                    |
| ••  |                       | APPLIC   | ANT: Y            | APPLICANT: Yang Wang,                                  |        | ichael W. Spellman                 |                    |
| ٠   |                       | NIMBER   | OF SE             | OTTENCES                                               | 17.    | 20121212                           |                    |
|     |                       | CORRES   | SPONDENCE         | CE ADDRES                                              | 388:   |                                    |                    |
|     |                       | ~        | ADDRESSEE         | Ger                                                    | ente   | ech, Inc.                          |                    |
| ••  |                       | υ,       | STREET:           | 1 DNA                                                  | Way    |                                    |                    |

STREET: 1 DNA WAY
CITY: South San Francisco
STATE: California
COUNTRY: USA

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316 CAT 318
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 8
 1 MetProAlaGlySerTrpAspProAlaGlyTyrLeuLeuTyrCysProCysMetGlyArg 20
 1 ATGCCCCCGCGGGCTCCTGGGACCCGGCTGGTTACCTGCTCTACTGCCCCTGCATGGGGCGC 60
ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYBE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: OF
 RESULT 2
US-09-774-954-4
US-09-774-954-4
Squence 4, Application US/09774954
Fublication No. US20040241645Al
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Yang Wang, Michael W. Spellman
APPLICANT: Yang Wang, Michael W. Spellman
APPLICANT: VARIGNENCE: 17
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA WAY
CITY: South San Francisco
STRATE: California
COUNTRY: USA
 Length:
Matches:
Conservative:
Mismatches:
Indels:
 US-09-774-954-9 (1-61) x US-09-774-954-16 (1-1100)
 TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-774-954-16
 5.82e-40
353.00
100.00%
100.00%
 Percent Similarity:
Best Local Similarity:
Query Match:
 181 CAT 183
 61 His 61
 Alignment Scores:
Pred. No.:
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APPLICANT: Wyeth APPLICANT: William APPLICANT: Wyeth William APPLICANT: Wyeth William APPLICANT: Wyeth Would William APPLICANT: William APPLICANT: Would William APPLICANT: Would William APPLICANT: Would William APPLICANT: Would William APPLICATION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES FILE REPRENCE: 031896-043000 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT APPLICATION NUMBER: US/10/956,157
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
LENGTH: 1400
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winheatin (Genentech)
CURRENT APPLICATION NUMBER: US/09/774,954
FILING DATE: 30-Jan-2001
CILASSIFFICATION NUMBER: US/08/78,741
FILING DATE: 26-NOV-1997
APPLICATION NUMBER: US/08/78,741
FILING DATE: 26-NOV-1997
APPLICATION NUMBER: US/08/78,741
FILING DATE: 31-JAN-1997
APPLICATION NUMBER: US/08/78,741
FILING DATE: 31-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: SOODOda, Caid G
REGISTRATION NUMBER: 39,044
FREEFRENCE/DOCKET NUMBER: 91041P1
TELEPOWUNICATION INFORMATION:
TELEPOWUNICATION INFORMATION:
TELEPOWUNICATION INFORMATION:
SEQUENCE THRACTERISTICS:
TELENGTH: 1300 base pairs
TELENGTH: 1300 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TYPE: Nucleic Acid
STRANDEDNESS: Single
TYPE: Nucleic Acid
STRANDEDNESS: Single
TYPE: Nucleic Acid
STRANDEDNESS: Single
TYPE: US-09-774-954-4

US-09-774-954-4

TALE-40 MACCORE: Linear
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 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
 US-09-774-954-9 (1-61) x US-09-774-954-4 (1-1300)
 US-10-956-157-9986
US-10-956-157-9986
; Sequence 9986, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INPORMATION:
 7.1e-40
353.00
100.00%
100.00%
 TYPE: DNA
ORGANISM: Homo sapiens
 Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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```
21 PheGlyAsnGlnAlaAspHisPheLeuGlySerLeuAlaPheAlaLySleuLeuAsnArg
 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk compuTER: 1BM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Winbatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/774,954
FILING DATE: 30-Jan-2001
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
 Sequence 1, Application US/09774954
; Publication No. US20040241645A1
; Publication No. US20040241645A1
; Publication No. US20040241645A1
; Publication No. US2004024ESA1
; TITLE OF INVENTION: O-Fucosyltransferase
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
 Conservative:
Mismatches:
 APPLICATION NUMBER: US/08/978,741
FILING DATE: 26-NOV-1997
APPLICATION NUMBER: 08/792,498
FILING DATE: 31-0AN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REGISTRATION NUMBER: 39,044
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
 US-09-774-954-9 (1-61) x US-09-774-954-1 (1-1514)
 Length:
Matches:
 Indels:
 TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHRACTERISTICS:
LENGTH: 1514 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
 8.51e-40
353.00
100.00%
100.00%
 Percent Similarity:
Best Local Similarity:
Query Match:
 181 ČÁT 183
 61 His 61
 Alignment Scores:
 US-09-774-954-1
 US-09-774-954-1
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 8
 Sequence 4751, Application US/10956157
Publication No. US20050118625A1
GRNERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Woth
APPLICANT
APPLICATION NUMBER: US/10/956,157
CURRENT APPLICATION NUMBER: US/10/956,157
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: PatentIn version 3.2
 132
 178
 133 ACCTTGGCTGTCCTCCTTGGATTGAGTACCAGCATCACAAGCCTCCTTTCACCAACCT 192
 40
 40
 41 ThrLeuAlaValProProTrpIleGluTyrGlnHisHisLysProProPheThrAsnLeu 60
 20
 72
 21 PheGlyAsnGlnAlaAspHisPheLeuGlySerLeuAlaPheAlaLysLeuLeuAsnArg
 Met ProAlaGlySerTrpAspProAlaGlyTyrLeuLeuTyrCysProCysMetGlyArg
 21 PheGlyAsnGlnAlaAspHisPheLeuGlySerLeuAlaPheAlaLysLeuLeuAsnArg
 1 MetProAlaGlySerTrpAspProAlaGlyTyrLeuLeuTyrCysProCysMetGlyA
 1506
61
0
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 Length:
Matches:
Conservative:
Mismatches:
Indels:
 Length:
Matches:
Conservative:
Mismatches:
Indels:
 US-09-774-954-9 (1-61) x US-10-956-157-4751 (1-1506)
 US-09-774-954-9 (1-61) x US-10-956-157-9986 (1-1400)
 Gaps:
 8.45e-40
353.00
100.00%
100.00%
 7.75e-40
353.00
100.00%
100.00%
 TYPE: DNA
ORGANISM: Homo sapiens
US-10-956-157-4751
 Percent Similarity:
Best Local Similarity:
Query Match:
DB:
 Percent Similarity:
Best Local Similarity:
Query Match:
 193 CAT 195
 CAT 301
 61 His 61
 61 His 61
 US-10-956-157-4751
JS-10-956-157-9986
 Alignment Scores:
Pred. No.:
 SEQ ID NO 4751
LENGTH: 1506
 Alignment Scores
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41 ThrLeuAlaValProProTrpIleGluTyrGlnHisHisHsLysProProPheThrAsnLeu 60
 COMPUTER READALE FORM:

MEDIUW TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: 18M PC compatible COMPUTER: 18M PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genetech)

CURRENT APPLICATION NUMBER: US/09/774,954

RILING DATE: 30-3an-2001

FILING DATE: 30-3an-2001

FILING DATE: 26-NOV-1997

APPLICATION NUMBER: US/08/978,741

FILING DATE: 31-3AN-1997

ATTORNEY/AGENT INPORMATION:

NAME: SYODOGA, CTAIG G

REGISTRATION NUMBER: 39,044

REFERENCE/DOCKET NUMBER: P1041P1

TELECOMUNICATION NUMBER: 39,044

TELECOMUNICATION NUMBER: 39,044

TELECOMUNICATION INPORMATION:

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TELECOMUNICATION INPORMATION:

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 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
 US-09-774-954-9 (1-61) x US-10-956-157-4752 (1-5218)
 LENGTH: 11284 base pairs
, NUMBER OF SEQ ID NOS: 319805
; SOFWHARE: Petentin version 3.2
; SEQ ID NO 4752
; LENGTH: 5218
 3.7e-39
353.00
100.00%
100.00%
 ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-956-157-4752
 Percent Similarity:
Best Local Similarity: 1
Query Match:
 299 CAT 301
 61 His 61
 Alignment Scores:
 No.
 RESULT 8
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 Sequence 4752, Application US/10956157
Publication No. US20050118625A1
GENERAL INFORMATION:
APPLICANT: Wounts, William
TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
FILE REFERENCE: 031896-043000 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT FILING DATE: 2004-10-04
 179 TITGGGAACCAGGCCGATCACTTCTTGGGCTCTCTGGCATTTGCAAAGCTGCTAAACCGT 238
 21 PheGlyAsnGlnAlaAspHisPheLeuGlySerLeuAlaPheAlaLysLeuLeuAsnArg 40
 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
 US-09-774-954-9 (1-61) x US-10-301-822-168 (1-5218)
 3.7e-39
353.00
100.00%
100.00%
 ; NAME/KEY: CDS
; LOCATION: (50)...(1216)
US-10-301-822-168
 TYPE: DNA
ORGANISM: Homo Sapiens
 Percent Similarity:
Best Local Similarity: 1
Query Match:
 299 CAT 301
 61 His 61
 RESULT 7
US-10-956-157-4752
 Alignment Scores:
Pred. No.:
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 Sequence 7, Application US/09774954
Sequence 7, Application US/09774954
Publication No. US20040241645A1
GENERAL INFORMATION:
APPLICANT: Yang Wang, Michael W. Spellman
TITLE OF INVENTION: O-Fucosyltransferase
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESSE:
STREET: 1 DNA Way
CITY: South San Francisco
STREET: California
 Conservative:
Mismatches:
Indels:
 US-09-774-954-9 (1-61) x US-11-097-143-18161 (1-1209)
 Mismatches:
Indels:
Gaps:
 US-09-774-954-9 (1-61) x US-09-774-954-7 (1-5009)
 Length:
Matches:
 TOPOLOGY: Linear SEQUENCE DESCRIPTION: SEQ ID NO: 7:
 LENGTH: 5009 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
 SEQUENCE CHARACTERISTICS
 202 TGGGTGGAGTATCGT 216
 6.29e-20
218.00
100.00%
100.00%
 47 TrpileGluTyrGln 51
 COUNTRY: USA
 Best Local Similarity:
Query Match:
DB:
 Best Local Similarity:
Query Match:
DB:
 Percent Similarity:
 Alignment Scores:
 US-09-774-954-7
 US-09-774-954-7
 Pred. No.:
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 4356 ACCTIGGCIGCCCTCCTIGGAIIGAGFACCAGCAICACAAGCCTCCTTICACCAACCIC 4415
 21 PheGlyAsnGlnAlaAspHisPheLeuGlySerLeuAlaPheAlaLysLeuLeuAsnArg 40
 41 ThrLeuAlaValProProTrpIleGluTyrGlnHisHisLysProProPheThrAsnLeu 60
 1 MetProAlaGlySerTrpAspProAlaGlyTyrLeuLeuTyrCysProCysMetGlyArg
 OR MORE
 APPLICANT: CELLAI.

APPLICANT: CELAI.

TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID

TITLE OF INVENTION: DREADS.

TITLE OF INVENTION: DREADS.

TITLE OF INVENTION: DREADS.

FILE REFERENCE: CLOOO728

CURRENT APPLICATION NUMBER: US/11/097,143

CURRENT FILING DATE: 1999-10-05

PRIOR FILING DATE: 1999-10-05

PRIOR PELICATION NUMBER: 60/160,191

PRIOR APPLICATION NUMBER: 60/161,91

PRIOR APPLICATION NUMBER: 60/164,769

PRIOR PILING DATE: 1999-10-28

PRIOR PILING DATE: 1999-11-22

PRIOR PLILING DATE: 1999-11-22

PRIOR PLILING DATE: 1999-11-22

PRIOR PLILING DATE: 1999-11-24

PRIOR PLILING DATE: 1999-11-24

PRIOR PLILING DATE: 2000-01-12

PRIOR APPLICATION NUMBER: 60/15,693

PRIOR PLILING DATE: 2000-01-12

PRIOR PLILING DATE: 2000-03-23

NUMBER OF SEQ ID NOS: 43008

SEQ ID NO 18161

LENGTH: 1209

SEQ ID NO 18161

LENGTH: 1209
 Length:
Matches:
Conservative:
 Length:
Matches:
Conservative:
 Mismatches:
Indels:
Gaps:
 US-09-774-954-9 (1-61) x US-09-774-954-5 (1-11284)
TYPE: Nucleic Acid

STRANDEDNESS: Single

TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-09-774-954-5
 Sequence 18161, Application US/11097143
Publication No. US20050208558A1
GENERAL INFORMATION:
APPLICANT: Venter, J. Craig
APPLICANT: et al.
 2.25e-21
223.00
91.11%
 9.25e-39
353.00
100.00%
100.00%
 TYPE: DNA
ORGANISM: DROSOPHILA
US-11-097-143-18161
 Percent Similarity:
Best Local Similarity:
Query Match:
 4416 CAT 4418
 61 His 61
 Percent Similarity:
 Alignment Scores:
Pred. No.:
 Alignment Scores:
Pred. No.:
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142 CACTICCIGGGAICALIGGCCTICGCCAAGGCGCTIAAICGCACCCIGAICCIGCCGCCG 201
 27 HisPheteuGlySerLeuAlaPheAlaLysLeuLeuAsnArgThrLeuAlaValProPro
7 AspProAlaGlyTyrLeuLeuTyrCysProCysMetGlyArgPheGlyAsnGlnAlaAsp
 COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/09/774,954
FILING DATE: 30-Jan-2001
CLASSIFICATION - CURKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/978,741
FILING DATE: 31-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: SYODOGA CRAIG G
RECISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: 39,044
REFERENCE/DOCKET NUMBER: 91041P1
TELECHOMONICATION INFORMATION:
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Percent Similarity:
Best Local Similarity:
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US-LILO97-143-18160/C

Publication No. US200502085581

Publication No. US200502085581

Publication No. US200502085581

APPLICANT: Vertex, J. Craig

APPLICANT: Vertex, J. Craig

TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID

TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID

TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID

TITLE OF INVENTION: DETECTION WIT, SUCH AS NUCLEIC ACID

TITLE OF INVENTION: DETECTION WIT, SUCH AS NUCLEIC ACID

TITLE OF INVENTION: DETECTION WIT, SUCH AS NUCLEIC ACID

FILE REFERENCE: CL000728

CURRENT APPLICATION NUMBER: 60/15/932

PRIOR PLICATION NUMBER: 60/16/191

PRIOR FILING DATE: 1999-10-18

PRIOR FILING DATE: 1999-10-18

PRIOR FILING DATE: 1999-11-12

PRIOR PLICATION NUMBER: 60/14/769

PRIOR PLICATION NUMBER: 60/173,383

PRIOR PLING DATE: 1999-11-12

PRIOR PLING DATE: 1999-11-12

PRIOR FILING DATE: 1999-11-12

PRIOR PLING DATE: 1999-11-13

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PRIOR PLING DATE: 1999-11-13

PRIOR
 2123 GAAAAACGACAACTAAAACGGGGGTTTTTCAAAGGACGCTTTTGGCAACCAGGCCGACCACTT 2064
 2063 CCTGGGATCATTGGCCTTCGCCAAGGCGCTTAATCGCACCCTGATCCTGCCGCGTGGGT 2004
 28 eLeuGlySerLeuAlaPheAlaLysLeuLeuAsnArgThrLeuAlaValProProTrpIl 48
-----GlyArgPheGlyAsnGlnAlaAspHisPh
 Length:
Matches:
Conservative:
Mismatches:
Indels:
 US-09-774-954-9 (1-61) x US-11-097-143-18160 (1-3264)
 7.17e-16
188.00
64.06%
59.38%
53.26%
 :||||||:::
2003 GGAGTATCGT 1994
 48 eGluTyrGln 51
 19 -----
 TYPE: DNA ORGANISM: DROSOPHILA
 Percent Similarity:
Best Local Similarity:
 RESULT 12

US-11-097-143-18082/c
 US-11-097-143-18160
 Alignment Scores:
Pred. No.:
 Best Local S
Query Match:
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| Pablication | Decision `

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Alignment Scores:
Pred. No.:
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                                                                                                                                            Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MetProAlaGlySerTrpAspProAlaGlyTyrLeuLeuTyrCysProCysMetGlyArg 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 236, Application US/10820474A

Sequence 236, Application No. US20050155089A1

GENERAL INFORMATION:
APPLICANT: LAL, PREETI
APPLICANT: GORGOR, GINA A.
APPLICANT: GORGOR, GINA A.
APPLICANT: GUEGLER, KARL J.
APPLICANT: GUEGLER, MEIL C.
APPLICANT: AKERBLOM, INGRID E.
APPLICANT: AKERBLOM, INGRID E.
APPLICANT: AKERBLOM, INGRID E.
APPLICANT: AKERBLOM, INGRID E.
APPLICANT: AND TOUNG, JANICE
APPLICANT: YUE, HENRY
APPLICANT: PATTERSON, CHANDRA
APPLICANT: BANDMAN, OLGA
TITLE OF INVENTION: SIGNAL PEPTIDE-CONTAINING MOLECULES
TITLE OF INVENTION SIGNAL PEPTIDE-CONTAINING MOLECULES
TITLE OF INVENTION SIGNAL PEPTIDE-CONTAINING MOLECULES
CURRENT APPLICATION NUMBER: US/10/820,474A

CURRENT APPLICATION NUMBER: US/10/820,474A
                                                                                                                                                                                                                                                                                                                                                                                                                                         521
19
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Matches:
Conservative:
Mismatches:
Indels:
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NAMBKEX: misc_feature
OTHER INFORMATION: Incyte Clone No: 1647884
15-10-820-4744-236
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR PILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 602444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | COURTRAIN FILING DATE: 2004-01-05
| PRIOR FILING DATE: 2001-03-05
| PRIOR FILING DATE: 2001-03-05
| PRIOR APPLICATION NUMBER: PCT/US99/14484
| PRIOR APPLICATION NUMBER: PCT/US99/14484
| PRIOR FILING DATE: 1998-06-26
| PRIOR FILING DATE: 1998-06-26
| PRIOR FILING DATE: 1998-07-31
| PRIOR FILING DATE: 1998-07-31
| PRIOR APPLICATION NUMBER: 60/102,686
| PRIOR FILING DATE: 1998-10-01
| NUMBER OF SEQ ID NOS: 269
| SEQ ID NO 236
| LENGTH: 760
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100.00$
95.00$
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                      TYPE: DNA
CORGANISM: Homo sapiens
US-09-925-065A-602444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-820-474A-236
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Pred. No.:
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A PAPLICANT: HALLAL, DAVID K.

A PAPLICANT: HALLAL, DAVID K.

A PAPLICANT: HALLAL, DAVID K.

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ITITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL CURRENT APPLICATION NUMBER: US 60/180,312

REIOR APPLICATION NUMBER: US 60/180,312

REIOR PELING DATE: 2000-02-04

REIOR PELING DATE: 2000-02-04

REIOR PELING DATE: 2000-03-27

REIOR PELING DATE: 2000-03-27

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REIOR PELING DATE: 2000-03-27

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REIOR PELING DATE: 2001-03-36

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REIOR PELING NUMBER: CT/USO1/0660

REIOR APPLICATION NUMBER: CT/USO1/0660

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REIOR APPLICATION NUMBER: CT/USO1/0660

REIOR APPLICATION NUMBER: CT/USO1/066
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SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                    US-09-774-954-9 (1-61) x US-10-820-474A-236 (1-760)
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FEATURE:
OTHER INFORMATION: MAP TO AC004624.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 9418, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Pennere Manach, David R.
                                           120.00
100.00%
95.00%
33.99%
                                                                                  Percent Similarity:
Best Local Similarity:
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27 ------HisPheLeuGlySerLeuAlaPheAlaLysLeuLeuAsn 39
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.2

OTHER INFORMATION: EXPRESSED IN HERRAT, SIGNAL = 2.3

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 4.3

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.2

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.3

OTHER INFORMATION: EXPRESSED IN BOME WARROW, SIGNAL = 1.9

OTHER INFORMATION: EXPRESSED IN PETAL LIVER, SIGNAL = 4.4

US-09-664-761-9418
                                                                                                                                         591
21
7
18
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2
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                    40 ArgThrLeuAlaValProProTrp 47
                                                                                                                                        0.00889
90.00
41.18%
30.88%
25.50%
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Score:
Percent Similarity:
Query Match:
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Search completed: October 26, 2005, 16:00:15 Job time : 272.326 secs

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Title: Perfect score:

Sequence:

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Scoring table:

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Sequence 13358, A
Sequence 2, Appli
Sequence 1, Appli
Sequence 12216, A
Sequence 14021, A
Sequence 10, Appl
                                                                                                                                                                                                                                                                                                                                  Sequence 3, Appli
Sequence 17224, A
Sequence 16800, A
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ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,741
FILING DATE: 26-No. 6100076-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/792498
FILING DATE: 31
ATTORNEY/AGENT INFORMATION:
NAME: SYODOGA, CTail G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: 39,044
REFERENCE/DOCKET NUMBER: 39,044
TELECOMMUTCATION INFORMATION:
TELEPHONE: 650/225-1489
TELEPHONE: 650/255-1489
              3 US-09-103-840A-1

3 US-09-103-840A-1

3 US-09-940-016-14021

US-09-949-016-14021

US-08-208-899A-1

US-08-434-151-1

US-08-675-773B-5

US-08-675-773B-5

US-08-675-773B-5

US-08-675-773B-5

US-08-675-773B-5

US-08-694-16-531-5

US-08-694-16-16-041

US-09-949-016-16-041

US-09-949-016-16-041

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US-09-949-016-16-041

US-09-949-016-16-041

US-09-949-016-11652

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US-09-949-016-11652

US-09-949-016-11652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 16, Application US/08978741
; Sequence 16, Application US/08978741
; Patent No. 610076
; GENERAL INFORMATION:
   TITLE OF INVENTION: O-PLOGSYLTANSferase
; TITLE OF INVENTION: O-PLOGSYLTANSferase
; CORRESPONDENCE ADDRESS:
   ADDRESSEE: Genencech, Inc.
   STREET: 1 DNA May
   CITY: South San Francisco
; STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
               4403765
4411529
36759
36759
1939
11136
11155
4 11155
4 11194
4 33373
4 3373
                                                                                                                                                                                                                                                                                                                                                                                                                                                             321022
40429
421491
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26896
1029
87644
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                                                                                                       US-08-978-741-16
                                               65.5
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-MODEL=frame+ pln.model -DEV=xlh

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-G-cgnz_1/USFTO spool h/US097749554/runat_25102005_105433_6415/app_query.fasta_1.917

-D-cgnz_1/USFTO spool h/US09774954 cdn -Immando.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15

-MODE=LOCAL -OUTPMT=pto -NORM=ext -HEAPSIZE=500 -THR MINEN=0 -MAXLEN=200000000

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-NO_MARD -LARGEQUERY -NEG_SCORE=s0 -WAIT -DSPBLOCK=100 -LONGLOG

-DSW TIMBOUT=120 -WARN TIMBOUT=30 -THREAPSIS=1 -XGAPDP=10 -XGAPEXT=0.5 -FCAPOP=6

-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Sequence 16, Appli
Sequence 6, Appli
Sequence 1, Appli
Sequence 2, Appli
Sequence 5, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 12127, Aspli
Sequence 12127, Aspli
Sequence 12127, Aspli
Sequence 12127, Aspli
                                                                                                       October 26, 2005, 08:18:39 ; Search time 53.4846 Seconds (without alignments) 1866.199 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Description
                                                                                                                                                                                                    1 MPAGSWDPAGYLLYCPCMGR.....LAVPPWIEYQHHKPPFTNLH
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11: /cgn2_6/prodateal/lina/5A_COMB.seq:*
12: /cgn2_6/prodateal/lina/5B_COMB.seq:*
3: /cgn2_6/prodateal/lina/6A_COMB.seq:*
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5: /cgn2_6/prodateal/lina/PcTUS_COMB.seq:*
6: /cgn2_6/prodateal/lina/backfiles1.seq:*
                      GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                              nucleic search, using frame_plus_p2n model
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US-09-333-729A-16
US-09-333-729A-6
US-09-333-729A-6
US-08-978-741-1
US-09-333-729A-2
US-09-270-767-14353
US-09-270-767-14353
US-09-378-741-7
US-09-949-016-12127
US-09-949-016-16285
                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                          1202784 seqs, 818138359 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
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7.0
7.0
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Maximum DB seq length: 200000000
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14166, A 125, App 12805, A

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US-09-333-729A-16
Sequence 16, Application US/09333729A
Sequence 16, Application US/09333729A
Sequence 16, Application US/09333729A
Sequence No. 6270987
SEQUENCE NO. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No. 1800 No
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LENGTH: 1100 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-08-978-741-16
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ORGANISM: Homo Sapien
US-09-333-729A-16
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Best Local Similarity: 1
Query Match: 1
DB:
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Best Local Similarity:
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APPLICATION NUMBER: 08/792498
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Pred. No.:
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Conservative:
Mismatches:
Indels:
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Patent No. 6100076
GENERAL INFORMATION:
APPLICANT: Yang Wang, Michael W. Spellman TITLE OF INVENTION: O-FUCOSyltransferase NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Prancisco
STATE: California
COUNTRY: USA
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                                                                          GENERAL INFORMATION:
APPLICANT: Wang, Yang
APPLICANT: Wang, Yang
APPLICANT: Spellman, Michael W.
APPLICANT: Spellman, Michael W.
FILE REFERENCE: P1041P1D1-Substitute
CURRENT APPLICATION WUMBER: US/09/333,729A
CURRENT FILING DATE: 1999-06-15
PRIOR FILING DATE: 1997-11-26
NUMBER OF SEQ ID NOS: 21
LENGTH: 1300
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,741
FILING DATE: 26-NO. 6100076-1997
CLASSIPICATION: 435
PRIOR APPLICATION DATA:
                     US-09-333-729A-6; Sequence 6, Application US/09333729A; Patent No. 6270987
                                                                                                                                                                                                                                                                                                                                                      , OTHER INFORMATION: Plasmid insert.
US-09-333-729A-6
                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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COMPUTER READABLE FORM:
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21 PheGlyAsnGlnAlaAspHisPheLeuGlySerLeuAlaPheAlaLysLeuLeuAsnArg
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Patent No. 6270987
GENERAL INFORMATION:
APPLICANT: Wang, Yang
TITLE OF INVENTION: O-Fucosyltransferase
FILE REFERENCE: Plotalpill-Substitute
CURRENT APPLICATION NUMBER: US/09/333,729A
CURRENT FILING DATE: 1999-06-15
PRIOR APPLICATION NUMBER: US 08/798,741
PRIOR APPLICATION NUMBER: US 08/798,741
PRIOR APPLICATION NUMBER: US 08/798,741
SEQ ID NO 2
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FILING DATE: 31
ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P1041P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
                                                                                                 TELEPAX: 650/225-1489
TELEPAX: 650/225-981
INPORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
LENGTH: 1514 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
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ORGANISM: Homo Sapien
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Best Local Similarity:
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinParin (Genentech)
CURRENT APPLICATION DATES.
APPLICATION NUMBER: US/08/978,741
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| Patent No. 6100076
| Patent INFORMATION:
| APPLICANT: Yang Wang, Michael W. Spellman
| TITLE OF INFORTION: O-Fucosyltransferase
| TUNBER OF SEQUENCES: 17
| CORRESPONDENCE ADDRESS:
| ADDRESSEE Genentech, Inc. | STREET: 1 DNA Way
| CITY: South San Francisco
| STATE: California
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; ORGANISM: Drosophila melanogaster
US-09-270-767-14353
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Best Local Similarity:
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US-09-270-767-14353
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   21 PheGlyAsnGlnAlaAspHisPheLeuGlySerLeuAlaPheAlaLysLeuLeuAsnArg 40
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ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winderin (Genentech)
CURRENT APPLICATION DATA
PPLICATION NUMBER: US/08/978,741
FILING DATE: 26-No. 6100076-1397
CLASSIFICATION NUMBER: US/08/978,741
FILING DATE: 31
APPLICATION NUMBER: US/08/978
FILING DATE: 31
ATTORNEY/AGENT INFORMATION:
NAME: SVODOMA, CTA19 G.
FREISTRATION NUMBER: 91041P1
TELEPRAM: SOFO/225-1489
TELEPRAM: 650/225-1489
TELEPRAM: 650/225-1489
TELEPRAM: GSO/325-1489
TELEPRAM: SEG ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1128 ABSE PAIRE
TTRANBEDNESS: SINGLE
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Matches:
Conservative:
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; Sequence 5, Application US/08978741
; Patent No. 6100076
; GENERAL INFORMATION:
; APPLICANT: Yang Wang, Michael W. Spellman
; TITLE OF INVENTION: O-Pucosyltransferase
; NUMBER OF SEQUENCES:
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STRET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
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Patent No. 6703491
GENERAL INFORMATION:
GENERAL INFORMATION:
TILE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 14353
LENGTH: 1320
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Matches:
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APPLICANT: Spellman, Michael W.
TITLE OF INVENTION: O-Fucosyltransferase
FILE REFERENCE: P1041P1D1-Substitute
CURRENT APPLICATION NUMBER: US/09/333,729A
CURRENT FILING DATE: 1999-06-15
PRIOR APPLICATION NUMBER: US 08/798,741
PRIOR FILING DATE: 1997-11-26
NUMBER OF SEQ ID NOS: 21
SEQ ID NO 8
LENGTH: 5009
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FILING DATE: 26-No. 6100076-1997
CLASSIFICATION: 435
PRIOR APPLICATION UNDER: 31
ATORNEY/AGENT INPORMATION:
ATORNEY/AGENT INPORMATION:
NAME: S'ODOGA, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P1041P1
TELEPHONE: 650/225-1489
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GENERAL INFORMATION:
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ORGANISM: Homo Sapien
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Search completed: October 26, 2005, 15:52:24
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US-09-103-840A-2
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RESULT 13

RESULT 13

REQUENCE 11358 Application US/09949016

Sequence 11358 Application US/09949016

Sequence 11358 Application US/09949016

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TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF TITLE OF TILING DATE: 2000-04-14

CURRENT APPLICATION NUMBER: 60/241.755

PRIOR FILING DATE: 2000-10-20

PRIOR PLICATION NUMBER: 60/231,768

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SEQ ID NO 13358

LENGTH: 2060-47

TYPE: DNA

CREANISM: Human

US-09-949-016-13358
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US-09-103-840A-2
US-09-103-840A-2
Sequence 2, Application US/09103840A
Patent No. 62943D.
Patent No. 62943D.
Patent No. 62943D.
APPLICANT: WHITE, Owen R.
APPLICANT: WHITE, Owen R.
APPLICANT: WHITE, Owen R.
APPLICANT: WINTION: DANA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
ITILE OF INVENTION: DANA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
ITILE OF INVENTION: DANA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
ITILE OF INVENTION: US/09/103,840A
CURRENT PILLING DATE: 1998-06-24
CURRENT FILLING DATE: 1998-06-24
SOFTWARE: Patentin Ver. 2.1
LENGTH: 4403765
TYPE: DNA
CRANKINS: Mycobacterium tuberculosis
FEATURE:
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; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
    APPLICANT: FIEISCHWAN, Robert D.
    APPLICANT: FIEISCHWAN, Robert D.
    APPLICANT: FRASER, Claire M.
    APPLICANT: FRASER, Claire M.
    APPLICANT: FRASER, Claire M.
    APPLICANT: PRASER, .
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"n" bases at various positions throughout the sequence represent a, t, c or \boldsymbol{g}
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Job time : 1666.48 secs .

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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

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ALIGNMENTS
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ACH76865
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4 ABL13946
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3 AAZ98210
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AAK51260
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ABX36491
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Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

4390206 segs, 2959870667 residues

Searched:

0.5 7.0 7.0

Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext

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Scoring table:

US-09-774-954-9 353

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Sequence:

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Abd32843 Human can Abn59850 Novel hum Aat01082 2-Alpha-f Aaq98461 GDP-L-fuc

Ach76865 Human gen Aak84657 Human imm

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn2003cs:* geneseqn2003ds:* geneseqn2004as:* geneseqn2004bs:*

geneseqn2002as:*geneseqn2002bs:*geneseqn2003as:* 9: geneseqn2003bs:*

Geneseq 16Dec04:*
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		Description		Aav65632 Human hea	Acn40746 Tumour-as	Adf81754 Leukaemia	Aav65633 Plasmid c	Aak51510 Human pol	
SOMMAKIES		ID		AAV65632	5218 13 ACN40746	ADF81754	AAV65633	AAK51510	
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		Query Match Length DB					11284	5230	
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		Score		353	353	353	353	241.5	
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Homo sapiens.

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                                                                                                                                                                                                                                                                                      This DNA encodes a human heart O-fucosyltransferase that can glycosylate an epidermal growth factor (ESP) domain of a polypeptide with an activated O-fucose residue. Inhibitors of O-fucosyltransferase, e.g. mutants with increased affinity for the EFG domains, are used in diagnosis and treatment of conditions associated with overexpression of fucosyltransferase, to promote survival of sensory (retinal) neurons. Probes based on EGF domain polypeptide are used to detect gene amplification and expression. The expression can also be determined at the protein level using antibodies specific for O-fucosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MetProAlaGlySerTrpAspProAlaGlyTyrLeuLeuTyrCysProCysMetGlyArg 20
                                                                                                                                                                                    Human O-fucosyl:transferase able to glycosylate epidermal growth factor domains - useful for diagnosis and treatment of diseases involving overexpression of the enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tumour-associated antigenic target (TAT) cDNA DNA326813, SEQ 1D NO:5725.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tumour-associated antigenic target; TAT; human; overexpression; cancer; tumour; diagnosis; cell proliferative disorder; breast cancer; colorectal cancer; lung cancer; overtian cancer; liver cancer; central nervous system cancer; bladder cancer; pancreatic cancer; certical cancer; melanoma; leuksemia; hybridisation probe; chromosome identification; chromosome mapping; gene mapping; gene therapy; cytostatic; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ATGCCCGCGGGGTCCTGGGACCCGGCCGTTACCTGCTCTACTGCCCCTGCATGGGGCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21 PheGlyAsnGlnAlaAspHisPheLeuGlySerLeuAlaPheAlaLysLeuLeuAsnArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1514 BP; 320 A; 435 C; 411 G; 348 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                          Claim 9; Fig 12A; 90pp; English.
              31-JAN-1997; 97US-00792498.
26-NOV-1997; 97US-00978741.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.56e-37
353.00
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                                                                (GETH ) GENENTECH INC.
                                                                                                Spellman MW;
                                                                                                                                  WPI; 1998-437477/37.
P-PSDB; AAW80571.
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Best Local Similarity:
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Pred. No.:
                                                                                                Wang Y,
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The invention relates to human tumour-associated antigenic target (TAT) polypeptides, and their related nucleic acids. The TAT polypeptides are everexpressed in cancer tissues compared to normal tissues, and may thus serve as effective targets for the diagnosis and treatment of cancer in mammals. The invention also relates to nucleic acid and polypeptide in mammals. The invention also relates to nucleic acid and polypeptide in artibody specific for a TAT polypeptide; and methods specific for a TAT polypeptide; a peptide or organic acid, an antibody specific for a TAT polypeptide; peptide or organic antibodies, and methods and compositions for the treatment or artibodies, antagonists, binding molecules and compositions are useful for diagnosis of cancer in mammals. TAT polypeptides, nucleic acids, antibodies, antagonists, binding molecules and compositions are useful for diagnosing or treating a cell proliferative disorder associated with concreased TAT expression, particularly cancers such as breast cancer, oration ancer, oratical cancer, olds may further be useful cancer, nucleic acids may further be used as hybridistation probes, in chromosome and gene mapping, in chromosome identification and in gene therapy. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        238
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                                                                                                                                                                                                                                                                                              New tumor-associated antigenic target polypeptides and nucleic acids, useful in preparing a medicament for treating or detecting a proliferative disorder, e.g. breast, lung, colorectal, ovarian or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5218 BP; 1255 A; 1274 C; 1334 G; 1355 T; 0 U; 0 Other;
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Matches:
Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 5725; 7273pp; English.
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                                                                                                     29-SEP-2003; 2003WO-US028547
                                                                                                                                        02-OCT-2002; 2002US-0414971P
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353.00
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                                                                                                                                                                                                                                                                                                                                                      prostate cancer or tumor.
                                                                                                                                                                                                              Zhang Z, Zhou
                                                                                                                                                                         (GETH ) GENENTECH INC
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P-PSDB; ABM82223.
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Best Local Similarity:
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                                                                    15-APR-2004
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US-09-774-954-9 (1-61) x AAV65633 (1-11284)
                    RESULT 4
                                  AAV65633
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to a method (M1) for determining the subtype of leukaemia cells and whether a patient sample contains leukaemia cells. The method comprises determining the expression profile of a group of markers in a patient sample. The method is useful for determining the presence of leukaemia cells, its types or subtypes, and
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                                                                                                                                                                                                                                                                                                                                                                                                                            Determining the subtype of leukemia cells and whether a patient sample contains leukemia cells or other cells, useful for treating leukemia, comprises determining the expression profile of a group of markers in a patient sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ThrLeuAlaValProProTrpIleGluTyrGlnHisHisLysProProPheThrAsnLeu
                                                                                                                                                                                                                                                                                                                                                                Dugas M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MetProAlaGlySerTrpAspProAlaGlyTyrLeuLeuTyrCysProCysMetGlyArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5266 BP; 1280 A; 1278 C; 1331 G; 1346 T; 0 U; 31 Other;
                                                                                                                                                                                                                                                                                                                                                                Schnittger S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for the preparation of a medicament for treating leukaemia.
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Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 2310; 2938pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
                                                                                                               Cytostatic; Gene therapy; leukaemia; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-774-954-9 (1-61) x ADF81754 (1-5266)
                                                                                     Leukaemia-related DNA sequence #2310.
                                                                                                                                                                                                                                                                                  (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
(UYLU-) UNIV LUDWIG MAXIMILIANS.
HARPE/) HAFBRLACH T.
(SCHOL) SCHOCH C.
                                                                                                                                                                                                                                                                                                                                                                Haferlach T, Schoch C, Kern W, I
Eils R, Brors B, Mergenthaler S;
          ADF81754 standard; DNA; 5266 BP
                                                                                                                                                                                                                                               05-NOV-2001; 2001EP-00126244.
                                                                                                                                                                                                                     04-NOV-2002; 2002WO-EP012303
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                                                                                                                                                                   WO2003039443-A2
                                                                                                                                                                                                                                                                                                                                       KERN W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
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                                                             26-FEB-2004
                                                                                                                                                                                             15-MAY-2003
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(KERN/) P
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This represents the mucleotide sequence of the plasmid construct used for the expression of human heart O-fucosyltransferase. The human O. Bethermal growth factor (BGF) domain of a polypeptide with an activated O-fucose residue. Inhibitors of O-fucosyltransferase, e.g. mutants with increased affinity for the BFG domains, are used in diagnosis and treatment of conditions associated with overexpression of O-fucosyltransferase, to promote survival of sensory (retinal) neurons. Probes based on EGF domain polypeptide are used to detect gene amplification and expression. The expression can also be determined at the protein level using antibodies specific for O-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human O-fucosyl:transferase able to glycosylate epidermal growth factor domains - useful for diagnosis and treatment of diseases involving overexpression of the enzyme.
                                                                                                                                                                                                                                 /______insert coding for human O-fucosyltransferase."
4218. .4235
/*tag= b
/note= "polyhistidine tag"
                                                                                                                        88.
                                                                                                       O-fucosyltransferase; epidermal growth factor; EGF; glycosylation; O-fucose; inhibitor; sensory neuron; retinal neuron; human; heart;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 11284 BP; 2947 A; 2602 C; 2624 G; 3111 T; 0 U; 0 Other;
                                                                              Plasmid construct for expression of human O-fucosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
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1140. .5333
**tag= a
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AAV65633 standard; DNA; 11284 BP
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                                                                                                                                                                                                                                                                                                                                                                 97WO-US023401
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Best Local Similarity:
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                                                                                                                                                     Homo sapiens.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                  17-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                             31-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                          26-NOV-1997;
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                                                                                                                                                                                                                                                                                                           WO9833924-A1
                                                     16-DEC-1998
                                                                                                                                                                                                                                                                                                                                       06-AUG-1998
                           AAV65633;
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220 GGGAACCAGGCCGATCATCTTGGGCTCTCTGGCATTTGCAAAGCTGCTAAACCGTACC 279
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(AAX52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication
                                                                                                                                                                                                                                                                                   22 GlyAsnGlnAlaAspHisPheLeuGlySerLeuAlaPheAlaLysLeuLeuAsnArgThr 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human, cytokine, cell proliferation, cell differentiation, gene therapy, vaccine, peptide therapy, stem cell growth factor, haematopoiesis, tissue growth factor, immunomodulatory, cancer, leukaemia, nervous system disorder; arthritis; inflammation, ss.
                                                                                                                                                                                                                            7 AspProAlaGlyTyrLeuLeuTyrCysProCysMet-------GlyArgPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xu C, Cao Y;
, Chen R, Wang
                                            Sequence 5230 BP; 1285 A; 1255 C; 1330 G; 1360 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Liu C, Drmanac RT, Asundi V, Zhou P, X
hao QA, Wang D, Wang J, Zhang J, Ren F,
Yang Y, Wejhrman T, Goodrich R;
                                                                                        Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                US-09-774-954-9 (1-61) x AAK51510 (1-5230)
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                                                                                                                                                                                                                                                                                                                                                                                                                                        BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-FEB-2000; 2000US-00496914.
27-AFR-2000; 2000US-00566875.
19-UJL-2000; 2000US-0059075.
19-SEP-2000; 2000US-00654936.
15-SEP-2000; 2000US-00654936.
20-CT-2000; 2000US-0063325.
30-NOV-2000; 2000US-00728422.
                                                                                                                                                                                                                                                                                                                                                                                                                                          AAK52494 standard; cDNA; 4850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-FEB-2001; 2001WO-US004098
                                                                                    1.87e-21
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P-PSDB; AAM79361.
                                                                                                                     Percent Similarity:
Best Local Similarity:
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Ma Y, Zhao QA, V
Xue AJ, Yang Y,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-NOV-2001
                                                                            Alignment Scores:
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                                                           4236 ATGCCCCCCGCGGCTCCTCGGACCCGGCCGGTTACCTGCTCTACTGCCCCTGCATGGGGCGCC 4295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to polynucleotides (AAKS1456-AAKS3435) and the encoded polypeptides (AAW7812-AAW80102) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopolesis regulating activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
                                                                                                                                                                                                                                                                                                                                                                                         Human, cytokine, cell proliferation, cell differentiation, gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZW;
   1 MetProAlaGlySerTrpAspProAlaGlyTyrLeuLeuTyrCysProCysMetGlyArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;
Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang :
Xue AJ, Yang Y, Wejhrman T, Goodrich R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 638-642; 6221pp; English.
                                                                                                                                                                                                                                                                                                                                                               Human polynucleotide SEQ ID NO 55.
                                                                                                                                                                                                                                                                          AAK51510 standard; cDNA; 5230 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-FBB-2000; 2000US-00496914.
27-APR-2000; 2000US-00560875.
20-UTN-2000; 2000US-00590075.
19-UTL-2000; 2000US-00654936.
15-SEP-2000; 2000US-0065543.
20-CCT-2000; 2000US-0063325.
30-NOV-2000; 2000US-00728422.
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                                                                                                                                                                                                                                                                                                                                    06-NOV-2001 (first entry)
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The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferentiation or which may induce production of other cytokines in other cell populations. The polymeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, nematopoiesis regulating activity tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: Records for SEQ ID NO 2110 (AAK52581) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication
                                                                                                                                                                                                                                                                                                                                                                                                                  279
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                                                                                                                                                                                                                                                                                                                                                                                                 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                         22 GlyAsnGlnAlaAspHisPheLeuGlySerLeuAlaPheAlaLyBLeuLeuAsnArgThr 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.
                                                                                                                                                                                                                                                                                                                                                                                               LeualaValProProTrpIleGluTyrGlnHisHisLysProProPheThrAsnLeuHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster expressed polynucleotide SEQ ID NO 36323.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                               Sequence 4850 BP; 1142 A; 1218 C; 1244 G; 1246 T; 0 U; 0 Other;
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Matches:
Conservative:
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11-JUL-2000; 2000US-00614150.
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229.50
80.00%
73.33%
65.01%
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P-PSDB; ABB69844.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (PEKE ) PE CORP NY
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Best Local Similarity:
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Pred. No.:
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLi6176-ABLi0511), expressed DNA sequences (ABLi6175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                           46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human O-fucosyl:transferase able to glycosylate epidermal growth factor domains - useful for diagnosis and treatment of diseases involving
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         O-fucosyltransferase; epidermal growth factor; EGF; glycosylation;
O-fucose; inhibitor; sensory neuron; retinal neuron; human; heart; ss.
                                                                                                                                                                                                                                                                                                                                                                                             7 AspProAlaGlyTyrLeuLeuTyrCysProCysMetGlyArgPheGlyAsnGlnAlaAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                         27 HispheleuGlySerLeuAlaPheAlaLysLeuLeuAsnArgThrLeuAlaValProPro
                                                                                                                                                                                                Sequence 1209 BP; 302 A; 313 C; 307 G; 287 T; 0 U; 0 Other;
Claim 1; SEQ ID NO 36323; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              First EcoRl nucleotide fragment of human KIAA0180.
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Mismatches:
Indels:
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Matches:
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223.00
91.11$
84.44$
63.17$
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                                                                                                                                                                                                                                                                                                                   Query Match:
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This represents a first EcoR1 nucleotide fragment of human KIAA0180. This 5009 basepairs partial cDNA encodes for a protein of unknown function from myeblast celline KG-1. The invention provides a human heart of ucosyltransferase that can glycosylate an epidermal growth factor (EGF) domain of a polypeptide with an activated o-fucose readule. Inhibitors of O-fucosyltransferase, e.g. mutants with increased affinity for the EFG domains, are used in diagnosis and treatment of conditions associated with overexpression of O-fucosyltransferase, to promote survival of sensory (retinal) neurons. Probes based on EGF domain polypeptide are used to detect gene amplification and expression. The expression can also be determined at the protein level using antibodies specific for O-fucosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is
                                                                                                                                                                                                                                                                                                                                                                                                  New isolated nucleic acid detection reagent for detecting 1000 or more
genes from Drosophila and for elucidating cell signaling and cell-cell
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                                                                                                                                                                                                              Sequence 5009 BP; 1235 A; 1195 C; 1268 G; 1311 T; 0 U; 0 Other;
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Matches:
Conservative:
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11-JUL-2000; 2000US-00614150.
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P-PSDB; ABB69843.
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Best Local Similarity:
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Pred. No.:
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2183 GATCCCAATGGCTACCTACTGTCGTGTATGGGTAAGTTTCACTTGGAAGCAACC 2124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                    2123 GAAAAACGACAACTAAAACCGCGCTTTTCAAAGGACGCTTTGGCAACCAGGCGGACCACTT
useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABBS7737-BBT2702). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                  -----GlyArgPheGlyAsnGlnAlaAspHisPh
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                                                                                                                                             Sequence 3264 BP; 904 A; 742 C; 758 G; 860 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                       7 AspProAlaGlyTyrLeuLeuTyrCysProCysMet------
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Mismatches:
Indels:
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Matches:
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11-JUL-2000; 2000US-00614150.
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188.00
64.06%
59.38%
53.26%
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2003 GGAGTATCGT 1994
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P-PSDB; ABB69791.
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Best Local Similarity:
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556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; signal peptide-containing protein; HSPP; diagnosis; cancer; inflammation; cardiovascular disease; anticancer; anti-inflammatory; antinatorbial; noctropic; neuroprotective; cardiovascular; hepatotropic; antiathmatic; gene therapy; cell proliferation; neurological disorder; reproductive disorder; developmental disorder; arteriosclerosis; cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia; asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia; parkinson's disease; Huntington's diseases; ovulatory defect;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48
        The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins (ABBS20717-ABB20072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   615 GAAAAACGACAACTAAACCGCGCTTTTCAAAGGACGCTTTGGCAACCAGGCCGACCACTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human signal peptide containing protein HSPP-102 cDNA SEQ ID NO:236
                                                                                                                                                                                        Sequence 3793 BP; 1020 A; 853 C; 950 G; 970 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                      7 AspProAlaGlyTyrLeuLeuTyrCysProCysMet------
                                                                                                                                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
Indels:
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98US-0094983P.
98US-0102686P.
98US-0112129P.
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188.00
64.06%
59.38%
53.26%
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GGAGTATCGT 486
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                                                                                                                                                                                                                                                                                           Similarity:
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01-OCT-1998;
11-DEC-1998;
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Pred. No.:
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AAZ98210
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huzogenote containing proteins HSPP-1 to HSPP-134. HSPPB have human signal peptide-containing proteins HSPP-1 to HSPP-134. HSPPB have human signal peptide-containing proteins HSPP-1 to HSPP-134. HSPPB have anticantered mitianterobial, nootropic, hepatotropic, negator control of HSPP sea beed to aradiovascular and antiasthmatic activities, and can be used in gene therapy. HSPPB can be used to treat or prevent disorders associated with decreased activity or function of HSPP. Such diseases include cell proliferation activity or function of HSPP. Such diseases include cell proliferation (including cancer), inflammation, cardiovascular, neurological, creproductive or developmental disorders (e.g. arteriosclerosis, cirrhosis, psoriasis, acquired immume deficiency syndrome, anaemia, asthma, Crohn's disease, microbial or other infections, congestive or ischemic heart disease, Alzheimer's, Parkinson's or Huntington's creatischemic activity disease, schizophrenia, ovulatory defects, muscular dystrophy). HSPP concleic acids can be used for the recombinant production of HSPP, for detecting HSPP in standard hybridisation and amplification assays (for detecting HSPP in standard hybridisation and amplification assays (for caribosyme therapeutics, for detecting related sequences or genetic variations, and for chromosomal mapping, HSPP are also used to raise (potential therapeutic agents). As are used to diagnose, or monitor, HSPP related diseases (in usual immunoassays) as therapoutic antagonists, in competitive drug screens, and for purification of HSPP from natural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Met ProAlaGlySerTrpAspProAlaGlyTyrLeuLeuTyrCysProCysMetGlyArg 20
                                                                                                                                                                  New human signal peptide-containing proteins useful in treatment, prevention and diagnosis of e.g. cancer, inflammation and cardiovascular
                                GA, Corley NC, Guegler KJ, Baughn MR;
Yue H, Patterson C, Reddy R, Hillman JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cytostatic; Gene Therapy; cancer; leukemia; lymphoma; Human; ds.
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100.00%
95.00%
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                                                        Au-Young J,
(INCY-) INCYTE PHARM INC.
                                                                                                                WPI; 2000-160673/14.
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                                      Lal P, Tang YT,
Akerblom IE, Au
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22-JUL-2004.

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Alignment Scores:
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                                                                                                            New isolated cancer associated nucleic acids comprising at least 10 contiguous nucleotides, useful for diagnosing, preventing and/or treating cancers such as leukemia and lymphoma.
                                                                                                                                                                          The present invention relates to cancer associated sequences (ADQ97025-ADQ98004). The sequences are useful for the diagnosia, prevention and/or treatment of cancer, such as leukemia and lymphoma. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formate directly from WIPO at fit, wipo.int/pub/published_poc_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ------HisPheLeuGlySerLeuAlaPheAlaLysLeuLeuAsn 39
                                                                                                                                                                                                                                                                                                                                                                             2 ProAlaGlySerTrpAspProAlaGlyTyrLeu---LeuTyrCysProCysMetGlyArg 20
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                                                                                                                                                                                                                                                  Sequence 97081 BP; 23547 A; 23101 C; 24653 G; 25780 T; 0 U; 0 Other;
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Matches:
Conservative:
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Indels:
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         22-DEC-2003; 2003WO-US041389
                             27-DEC-2002; 2002US-00330773
                                                 (SAGR-) SAGRES DISCOVERY INC
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94.00
43.84%
28.77%
26.63%
                                                                      Malandro MS;
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                                                                                           4PI; 2004-543781/52
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Percent Similarity:
Best Local Similarity:
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                                                                      Morris DW,
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Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SRNPs are derived from human HeLe cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 ProbladlySerTrpAspProAlaGlyTyrLeu---LeuTyrCysProCysMetGlyArg 20
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04-FEB-2000; 2000US-0180312P.
26-MX-2000; 2000US-0207456P.
30-UIN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00533366.
21-SEP-2000; 2000US-023468PP.
27-SEP-2000; 2000US-023459P.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                             (MOLE-) MOLECULAR DYNAMICS INC.
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The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human feetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
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30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-0053-566.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-02359P.
04-OCT-2000; 2000GB-00024263.
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CHIS BROWK (1861.C)

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GenCore version 5.1.6
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- protein search, using sw model OM protein

Run on:

October 25, 2005, 15:21:43; Search time 7.64066 Seconds (without alignments) 768.157 Million cell updates/sec

Title: Perfect score:

US-09-774-954-9 353 1 MPAGSWDPAGYLLYCPCMGR......LAVPPWIEYQHHKPPFTNLH 61 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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A;Cross-references: EMBL:U41528; NID:g1109795; PID:g1109800; PIDN:AAA83156.1; CESP:C15C7. C;Genetics:
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hypothetical protein C15C7.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T15511
R;Leimbach, D.
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A;Introns: 31/3; 67/2; 106/2; 166/1; 202/3; 235/3; 364/3; 410/3
                                                                                                                           submitted to the EMBL Data Library, November 1995
A;Description: The sequence of C. elegans cosmid C15C7.
A;Reference number: Z18363
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A,Status: preliminary: translated from GB/EMBL/DDBJ
A,Molecule type: DNA
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A;Statuciss preliminary; translated from GB/EMBL/DDBJ A;Statucis preliminary; translated from GB/EMBL/DDBJ A;Statucis: 1-354 cREG> A;Cross-references: UNIPROT:P51474; GB:S75255; NID:g807171; PIDN:AAB32221.1; PID:g807172 A;Introns: 124/1; 180/2; 235/3; 315/3 C;Superfamily: vertebrate rhodopsin C;Keywords: chromoprotein; eye; G protein-coupled receptor; lipoprotein; phosphoprotein; F;299/Binding site: retinal (Lys) (covalent) #status predicted C;Species: Astyanax mexicanus (Mexican tetra) C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004 C;Accession: IS1266 R;Register, E.A.; Yokoyama, R.; Yokoyama, S. J. Mol. Evol. 39, 268-273, 1994 A;Title: Multiple origins of the green-sensitive opsin genes in fish. A;Reference number: I51266; MUID:95018302; PMID:7932788 Score 78; DB 2; Length 354; Pred. No. 0.046; green-sensitive - Mexican tetra 22.1%; 33.3%; Query Match Best Local Similarity A; Accession: I51266

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Nature 409, 1007-1011, 2001 A;Fitle: Massive gene decay in the leprosy bacillus. A;Releance number: As6909; MUID:21128732; PMID:11234002 A;Accession: B86968 A;Status: preliminary A;Accession: Bresidues: 1-223 acrossion: A;Residues: 1-223 acrossion: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: Backsion: Ba
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N.Alternate names: Bl17_Cl_19
C.Species: Mycobacterium leprae
C.Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C.Accession: S72721
R.Smith, D.R.; Robison, K.
R.Smith, D.R.; Robison, K.
R.Smith, D.R.; Robison, Mycobacterium leprae cosmid Bl177.
A.Reference number: S72694
A.Accession: S72721
A.Actus: preliminary
A.Actus: preliminary
A.Moseucie type: DNA
A.Residues: 1-219 < CMI>
A.Residues: 1-219 < CMI>
A.Ccoss_references: UNIPROT:Q49637; EMBL:U00011; NID:g466807; PIDN:AAA17085.1; PID:g4668)
                                                                                                                       A; Introns: 121/1; 177/2; 232/3; 312/3
C; Superfamily: vertebrate rhodopsin
C; Superfamily: vertebrate rhodopsin
C; Superfamily: vertebrate protein.
C; Reyords: chromoprotein; eye; G protein-coupled receptor; lipoprotein; phosphoprotein;
C; Reyords: chromoprotein; eye; G protein-coupled receptor; lipoprotein; phosphoprotein;
F; 256, Binding site: retinal (Lys) (covalent) #status predicted
F; 322, 323, Binding site: palmitate (Cys) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 18.7%; Score 66; DB 2; Length 355; Best Local Similarity 28.9%; Pred. No. 1.5; Matches 13; Conservative 10; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 YLLYCPCMGRFGNQADHFLGSLAFAKLLNRTLAVPPWIEYOHHKP 55
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Pred. No. 1.4;
4; Mismatches 11;
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C;Superfamily: conserved hypothetical protein H11648
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C,Superfamily: conserved hypothetical protein H11648
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Best Local Similarity 43.8%;
Matches 14; Conservative
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Matches 14; Conserv
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NyAlternate names: green visual pigment
C;Species: Gallus gallus (chicken)
C;Dpecies: Gallus gallus (chicken)
C;Dpecies: 31-0ec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Date: 31-0ec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Date: 31-0ec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Date: 31-0ec-1993 #sequence revision 31-Dec-1993 #text_change 09-Jul-2004
C;Date: 31-0ec-1993 #sequence revision 31-Dec-1993 #text_change 09-Jul-2004
Biochemistry 31, 3309-3315, 1992
A;Title: A visual pigment from chicken that resembles rhodopsin: amino acid sequence A;Reference number: A2347; MUID:92207951; PMID:1554715
A;Rolecule type: DNA
A;Rolecule type: DNA
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C;Species: Anolis carolinensis (green anole)
C;Species: Anolis carolinensis (green anole)
C;Accession: 15-139
B;Kawmura 5.; Yokoyama, 8.
B;Kawmura 5.; Yokoyama, 8.
A;Title: Paralogous origin of the rhodopsinlike opsin genes in lizards.
A;Title: Paralogous origin of the Rhodopsinlike opsin genes in lizards.
A;Reference number: 151319; MUID:95371134; PMID:7643409
A;Accession: 151319
A;Accession: 151319
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Redession: 151319
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Best Local Similarity 26.2%; Pred. No. 1.1;
Matches 17; Conservative 9; Mismatches 23; Indels 16; Gaps
       Gaps
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0
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       23; Indels
7; Mismatches
       15; Conservative
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       Matches
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A,Note: the authors translated the codon AAC for residue 195 as Glu
A,Note: the authors translated the codon AAC for residue 195 as Glu
C,Superfamily: vertebrate rhodopsin
C,Superfamily: vertebrate rhodopsin
C,Keywords: chromoprotein; eye; G protein-coupled receptor; glycoprotein; lipoprotein; pl
F)37-61/Domain: transmembrane #status predicted <TM1>
F)45-66/Domain: transmembrane #status predicted <TM3>
F)115-140/Domain: transmembrane #status predicted <TM4>
F)23-230/Domain: transmembrane #status predicted <TM4>
F)23-230/Domain: transmembrane #status predicted <TM5>
F)28-30/Domain: transmembrane #status predicted <TM5>
F)28-30/Domain: transmembrane #status predicted <TM7>
F)28-30/Domain: transmembrane #status predicted <TM7>
F)28-30/Domain: transmembrane #status predicted <TM7>
F)28-30/Domain: transmembrane #status predicted <TM7>
F)323-33/Binding site: carbohydrate (Asn) (covalent) #status predicted
F)322,323/Binding site: palmitate (Cys) (covalent) #status predicted
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                                                                                                                                                            A;Cross-references: UNIPROT:P32312; GB:L11866; NID:g212959; PIDN:AAA49169.1; PID:g212960 A;Experimental source: retina A;Note: sequence extracted from NCBI backbone (NCBIP:122266) (Superfamily: vertebrate rhodopsin C;Superfamily: vertebrate rhodopsin C;Keywords: chromoprotein; eye; G protein-coupled receptor; glycoprotein; lipoprotein; p? F;2,15/Binding site: carbohydrate (Asn) (covalent) #status predicted F;2,15/Binding site: retinal (Lys) (covalent) #status predicted
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A,Residues: 1-353 <HIS>
A,Cross-references: UNIPROT:P22671; GB:M63632; NID:9213348; PIDN:AAA49342.1; PID:9213349
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C;Species: Lampetra japonica (Japanese lamprey)
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
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R;Hisatomi, O.; Iwasa, T.; Tokunaga, F.; Yasui, A.
Biochem. Biophys. Res. Commun. 174, 1125-1132, 1991
A;Title: Isolation and characterization of lamprey rhodopsin cDNA.
A;Reference number: JN0120; MUID:91144585; PMID:1840482
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17.6%; Score 62; DB 1; Length 353; ilarity 31.9%; Pred. No. 4.8; Conservative 9; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  136 YIVVCKPMGSFKFSSTHASAGIAFTWVMAMACAAPPLVGWSRYIP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
17.6%; Score 62; DB 2; Length 349;
Best Local Similarity 26.7%; Pred. No. 4.8;
Matches 12; Conservative 9; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 YLLYCPCMGRFGNQADHFLGSLAFAKLLNRTLAVPPWIEYQHHKP 55
A; Reference number: A45229; MUID: 93120096; PMID: 8418840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: not compared with conceptual translation A;Molecule type: mRNA
                                                          A;Status: not compared with conceptual translation A;Molecule type: mRNA A;Residues: 1-349 <JOH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Experimental source: liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
les 15; Conserv
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                                           A;Accession: B45229
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Biochemistry 32, 208-214, 1993
A;Title: Cloning and expression of goldfish opsin sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: DNA
A;Residues: 1-212 <HEIJ c. AREJ C. AREJ C. AREJ C. AREJ C. AREJ C. AREJ C. AREJ C. AREJ C. AREJ C. AREJ C. AREJ C. AREJ C. A;Experimental source: serogroup O1; strain N16961; biotype El Tor
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R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J. B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
                                                                                                                                                                                                                                                                                                                                             R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J. chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, I. R.N.; Makalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
                                                                                                                                                                                                                  CbbY family protein VCA0662 [imported] - Vibrio cholerae (strain N16961 serogroup O1) C; Species: Vibrio cholerae C; Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004 C; Accession: D82431
                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Reference number: A82035; MUID: 20406833; PMID: 10952301
A; Reference number: A82035; MUID: 20406833; PMID: 10952301
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C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          opsin, green-sensitive (clone GFgr-2) - goldfish
C;Species: Carassius auratus (goldfish)
C;Date: 30-Apr_1993 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       conserved hypothetical protein CC0748 [imported] - Caulobacter crescentus C;Species: Caulobacter crescentus C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 PAGYLLYCPCMGR-----FGNQADHFLGSLAFAKLLNRTLAVPPWIEYQHHKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <u>ښ</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 64; DB 2; Length 212;
Pred. No. 1.5;
8; Mismatches 21; Indels
          17.7%;
ilarity 32.1%;
Conservative
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Best Local Similarity 35.2%;
Matches 19; Conservative
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Best Local Similarity
Matches 17; Conserv
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A;Gene: VCA0662
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Query Match 17.4%; Score 61.5; DB 2; Length 349; Best Local Similarity 30.2%; Pred. No. 5.5; Matches 13; Conservative 6; Mismatches 21; Indels

11 YLLYCPCMGRFGNOADHFLGSLAFAKLLNRTLAVPP---WIEY 50

RESULT 12 D95101

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hypothetical protein Rv2604c - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Accession: 070570
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Genles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome sheesenen number: A70500; MUID:98295987; PMID:9634230
A;Rocession: C70570
A;Accession: C70570
A;
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A;Accession: T41004
A;Status: pre-iminary; translated from GB/EMBL/DDBJ
A;Molecule: type: DNA
A;Residues: 1-492 < WOD.
A;Cross-references: UNIPROT:OG0077; EMBL:AL023776; PIDN:CAA19301.1; GSPDB:GN00067; SPDB:8
A;Experimental source: strain 972h-; cosmid c1494
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                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                10 GYLLYCPCMGRFGNQADHFLGSLAFAKLLNRTLAVPPWIEY 50
                                                               18;
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Pred. No. 14;
8; Mismatches
Best Local Similarity 36.6%; Pred. No. 17;
Matches 15; Conservative 5; Mismatches
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illarity 43.8%;
Conservative 4
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Best Local Similarity 41.2%;
Matches 14; Conservative
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A;Map position: 2
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es 14; Conserv
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cell division protein [imported] - Streptococcus pneumoniae (strain R6)
cell division protein [imported] - Streptococcus pneumoniae
Cispecies: Streptococcus pneumoniae
Cispecies: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
Cispecies: 189769
Cispecies: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
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Cipacies; Streptococcus pneumoniae
Cipacession: D95101
R; Tetelin, H; Nelson, K.E.; Paulsen, J.A.; Read, T.D.; Peterson, S.; Heid
On, J.D.; Umayam, L.A.; Multe, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,
nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-966, 2001
A; Tetle: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A; Reference number: A95000; MUID:21357209; PMID:11463916
A; Recession: D95101
A; Reterence Town A; Recession: D95101
A; Redevence Town A; Reference T
                                                 A,Cross-references: UNIPROT:P32311; GB:L11865; NID:g212957; PIDN:AAA49168.1; PID:g212958
A,Experimental source: retina
A,Styperimental source: retina
C,Superfamily: vertebrate from NCBI backbone (NCBIP:122265)
C,Superfamily: vertebrate rhodopsin
C,Superfamily: vertebrate rhodopsin
C,Superfamily: vertebrate rhodopsin
C,Keynords: protein-coupled faceptor; glycoprotein; lipoprotein; F:2.15,Painding site: carbohydrate (Asn) (covalent) #status predicted
F;296/Binding site: retinal (Lys) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SpoE family protein [imported] - Streptococcus pneumoniae (strain TIGR4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3;
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Query Match 17.1%; Score 60.5; DB 2; Length 767; Best Local Similarity 36.6%; Pred. No. 17; Matches 15; Conservative 5; Mismatches 18; Indels

A,Gene: SP0878 C,Superfamily: Bacillus subtilis DNA translocase spoIIIE

SP0878

142 GVALYIPTAFLFSNIGTYFIGSIL---ILVGSLLVSPWSVY 179

10 GYLLYCPCMGRFGNQADHFLGSLAFAKLLNRTLAVPPWIEY

ò

17.1%; Score 60.5; DB 2; Length 767;

Query Match

A,Gene: ftsK C,Superfamily: Bacillus subtilis DNA translocase spoIIIE

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Sequence 169, App
Sequence A Appli
Sequence 18162, A
Sequence 18162, A
Sequence 17, Appli
Sequence 8, Appli
Sequence 102, Appli
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Sequence 14, Appl
Sequence 327031,
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Sequence 2, Appli
                                                                                                                                                   October 25, 2005, 15:22:39; Search time 35.8234 Seconds (without alignments) 710.936 Million cell updates/sec
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1 MPAGSWDPAGYLLYCPCMGR.....LAVPPWIEYQHHKPPFTNLH
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6/prodate 1/2 pubpas/0809A_PUBCOMB.pep: *
6/prodate 1/2 pubpas/0809B_PUBCOMB.pep: *
6/prodate 1/2 pubpas/0809C_PUBCOMB.pep: *
6/prodate 1/2 pubpas/0810A_PUBCOMB.pep: *
6/prodate 1/2 pubpas/0810B_PUBCOMB.pep: *
6/prodate 1/2 pubpas/0810B_PUBCOMB.pep: *
6/prodate 1/2 pubpas/0810C_PUBCOMB.pep: *
6/prodate 1/2 pubpas/0810C_PUBCOMB.pep: *
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1: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*

7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*

8: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*

9: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*

10: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-774-954-2
US-10-301-822-169
US-09-774-954-6
US-09-774-954-3
US-11-097-14-954-1
US-09-774-954-1
US-09-774-954-1
US-09-774-954-102
US-09-774-954-1102
US-09-774-954-1102
US-09-774-954-1102
US-09-774-954-1102
US-10-425-115-327031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1862994 segs, 417510619 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                      OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length DB
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Perfect score:
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ALIGNMENTS

Sequence 266118,	equenc	Sequence 113919,	Sequence 12551, A	Sequence 63705, A	Sequence 62907, A	eguenc	equenc	equenc	edneuc	equenc	ednenc	eguenc	eguenc	edneuc	equence 233161	equence 1698,	Sequence 3610, Ap	13343,	equence 13598,	96	Seguenc	quence 2, Ag	Sequence 174345,	Sequence 49507, A	Sequence 195444,	Sequence 61790, A	equence 62362,	Sequence 64'	quence 17,		equence 47	equence 17	Sequence 104, App	
US-10-424	US-10-425-115-20132	US-10-437-963-11391	US-10-156-761-1255	US-10-282-122A-637	US-10-282-122A-6290	US-10-369-493-828	US-10-425	6 US-10-437-963-18006	6 US-10-856-499-2	6 US-10-437-963-1	5 US-10-424-599-1	6 US-10-437-963-1	6 US-10-437-963-19868	6 US-10-425-115-	5 US-10-424-599-23316	7 US-10-472-928-	0 - 361	-1334	1359	7-9	2A-	9 US-09-775-978-2	9-1743	4-49	9-19544	2A-6179	2A-6236	2A-6	A-1	4 US-10-282-837-1	4 US-10-225-567A-	4 US-10-145-586-1	4 US-10-241-2	
152	189	538	601	223	191	580	156	1271	412	119	543	1262	75	117	146	741	763	767	167	767	767	783	545	557	169	198	198	198	398	398	398	398	398	
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RESULT 1

US-09-774-954-9

Sequence 9, Application US/09774954

Publication No. US20040241645A1

GENERAL INFORMATION:

APPLICANT: Yang Wang, Michael W. Spellman

TITLE OF INVENTION: O-Pucosyltransferase

NUMBER OF SEQUENCES: 17

CORRESPONDENCE SES:

ADDRESSEE: Genethech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STARTE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBW PC compatible

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COMPUTER: IBW PC compatible

COMPUTER: IBW PC compatible

COMPUTER: IBW PC compatible

MEDIUGATION NUMBER: US/09/774,954

FILING DATE: 30-Jan-2001

CLASSIFICATION NUMBER: 08/792,498

FILING DATE: 31-JAN-1997

APTORINEY/AGENT INFORMATION:

NAME: Svoboda, Craig G.

RESERBENCE/DOCKET NUMBER: P1041P1

TELECOMMUNICATION INFORMATION:

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1 MPAGSWDPAGYLLYCPCMGRFGNQADHFLGSLAFAKLLNRTLAVPPWIEYQHHKPPFTNL 60
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COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: Wirbatin (Genentech)
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100.0%; Score 353; DB 14;
Best Local Similarity 100.0%; Pred. No. 1.7e-36;
Matches 61; Conservative 0; Mismatches 0;
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US-00-774-954-6

10S-00-774-954-6

1 Sequence 6, Application US/09774954

1 Publication No. US20040241645A1

1 Publication No. US20040241645A1

1 PUBLICANT: Yang Wang, Michael W. Spellman

1 TILE OF INVENTION: O-Pucosyltransferase

1 CORRESPONDENCE ADDRESS:

1 CORRESPONDENCE ADDRESS:

2 STREET: 1 DNA Way

2 TITE: California

2 COUNTRY: California

2 COUNTRY: California
                                                                                                                                                                                                 Sequence 169, Application US/10301822
Publication No. US20030148410A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
CORGANISM: Homo Sapiens
US-10-301-822-169
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                                                                                                                                                                                                                                Length 61;
                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Winbatin (Genericch)

CURRENT APPLICATION NUMBER: US/09/774,954

FILING DATE: 30-Jan-2001

CLASSIFICATION: «Unknown»

PRIOR APPLICATION NUMBER: US/08/978,741

FILING DATE: 36-NOV-1997

APPLICATION NUMBER: US/08/978,741

FILING DATE: 31-JAN-1997

ATTORREY/AGENT ITON NUMBER: 08/792,498

FILING DATE: 31-JAN-1997

ATTORREY/AGENT ITON NUMBER: 99,044

REGISTRATION NUMBER: 99,044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 2
US-09-774-954-2
US-09-774-954-2
Sequence 2. Application US/09774954
; Publication No. US20040241645A1
GENERAL INFORMATION:
TITLE OF INVENTION: O-FUCOSYLTANSFERASE
NUMBER OF RECUENCES: 17
CORRESPONDENCE ADDRESS:
STREET: 1 DNA Way
CITY: South San Francisco
STRATE: California
COUNTRY: USA
                                                                                                                                                                                                                              Query Match 100.0%; Score 353; DB 11; Best Local Similarity 100.0%; Pred. No. 2.2e-37; Matches 61; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: P1041P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
TELEPAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 365 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-774-954-2
                                                                                                                             TOPOLOGY: Linear SEQUENCE DESCRIPTION: SEQ ID NO: 9: US-09-774-954-9
       TELEPHONE: 650/225-1489
                          INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 61 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                61 H 61
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y APPLICANT: Millennium Finarmaccenticate, ......
APPLICANT: Barger, Allison
APPLICANT: Barger, Allison
APPLICANT: Guillenette, Tracy L.
APPLICANT: Guillenette, Tracy L.
APPLICANT: Schlegel, Robert
APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John E.
APPLICANT: Monahan, John E.
APPLICANT: Hargart, Lawrence J.
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, THERAPY OF COLON CANCER
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, THERAPY OF COLON CANCER
TITLE OF INVENTION: THERAPY OF COLON CANCER
TITLE OF INVENTION: MUBBR: US 10/301,822
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 60/339,971
PRIOR APPLICATION NUMBER: US 60/331,988
PRIOR APPLICATION NUMBER: US 60/381,988
PRIOR PILING DATE: 2002-05-20
NUMBER OF SEQ ID NOS: 228
SEQ ID NOS: 228
LENGTH: 388
WANDER OF SEQ ID NOS: 228
LENGTH: 388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24 MPAGSWDPAGYLLYCPCMGRFGNQADHFLGSLAFAKLLNRTLAVPPWIEYQHHKPPFTNL
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RESULT 7

'US-09-774-954-17

'Sequence 17, Application US/09774954

; Publication No. US20040241645A1

; GENERAL INFORMATION:

APPLICANT: Yang Wang, Michael W. Spellman

TITLE OF INVENTION: O-Fucosyltransferase

'NUMBER OF SEQUENCES: 17

''THIRE OF INVENTION: O-Fucosyltransferase

''THIRE OF SEQUENCES: 17

''THIRE OF INVENTION: O-Fucosyltransferase
                                                                                                                                                                                       Score 295; DB 11;
Pred. No. 6e-30;
                                                                                                                                                                                                                                      0; Mismatches
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 18162
                                                                                           TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 18162, Application US/11097143 Publication No. US20050208558A1 GENERAL INFORMATION:
                                               LENGTH: 61 amino acids
TYPE: Amino Acid
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                    vuery match
Best Local Similarity 91.5%;
Matches 54; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity 84.4'
Matches 38; Conservative
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US-11-097-143-18162
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/774,954
FILING DATE: 30-Jan-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.0%; Score 353; DB 11; Best Local Similarity 100.0%; Pred. No. 1.7e-36; Matches 61; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Yang Wang, Michael W. Spellman
TITLE OF INVENTION: O-PROCOSyltransferase
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSES: Genentech, Inc.
STREET: 1 DNA WAY
CITY: South San Francisco
STATE: California
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/774,954
FILING DATE: 30-Jan-2001
CLASSIFICATION: «UNKNOWN»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/978,741
FILING DATE: 26-NOV-1997
APPLICATION NUMBER: 08/792,498
FILING DATE: 31-JAN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                            ATTURNES TO THE SECONDARY CRAIG G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P1041P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
TELEFAX: 650/225-1489
TELEFAX: 650/952-9881
INFORMATION POR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 397 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/978,741
FILING DATE: 26-NOV-1997
APPLICATION NUMBER: 08/792,498
FILING DATE: 31-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: SYODOGA, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P1041P1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-774-954-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/09774954
Publication No. US20040241645A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
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APPLICANT: Venter, J. Craig
APPLICANT: et al.
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: DESCOPHILA GENES.
TITLE OF INVENTION: DROSOPHILA GENES.
CURRENT APPLICATION NUMBER: 60/157, 832
PRIOR APPLICATION NUMBER: 60/160,191
PRIOR PILING DATE: 1999-10-05
PRIOR PILING DATE: 1999-10-28
PRIOR PILING DATE: 1999-10-28
PRIOR PILING DATE: 1999-11-12
PRIOR PILING DATE: 1999-11-12
PRIOR PILING DATE: 1999-11-12
PRIOR PILING DATE: 1999-10-28
PRIOR PILING DATE: 1999-10-28
PRIOR PILING DATE: 2000-01-12
PRIOR PILING DATE: 2000-01-12
PRIOR PILING DATE: 2000-01-12
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PRIOR PILING DATE: 2000-01-12
PRIOR PILING DATE: 2000-01-24
PRIOR PILING DATE: 2000-01-12
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PRIOR PILING DATE: 2000-01-14
PRIOR PILING DATE: 2000-01-15
PRIOR PILING DATE: 2000-01-14
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PRIOR PILING DATE: 2000-01-14
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                                                                                                                                                                  61
                                                                                                                                                                                                                  3 AGSWDLAGYLLXXPXMGRFGNQADHFLGSLAFAKLXVRTLAVPFWIEYQHHKPPFTNLH 61
                                                                                                                                                                  3 AGSWDPAGYLLYCPCMGRFGNQADHFLGSLAFAKLLNRTLAVPPWIEYQHHKPPFTNLH
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Length 61;
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84.4%; Pred. No. 7.9e-20;
tive 3; Mismatches 4;
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Gaps
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Pred. No. 6.1e-07;
5; Mismatches 6; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             166 GRFGNQVDQFLGVLAFAKALDRTLVLPNFIEFKH 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19 GRFGNQADHFLGSLAFAKLLNRTLAVPPWIEYQH 52
                                                                                                                                                                                                                                                                              TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ 1D NO: 8:
US-09-774-954-8
                 REGISTRATION NUMBER: 39,044
REGISTRATION NUMBER: 91,044
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
TELEPRANICATION INFORMATION: 81
INFORMATION FOR SEQ ID NO: 81
SEQUENCE CHARACTERISTICS:
                       39,044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 102, Application US/10820474A Publication No. US20050155089A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24 MPAGSWDPAGYLLYCPCMGK 43
                                                                                                                                                                                                                                     LENGTH: 474 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 34.8%;
Best Local Similarity 67.6%;
Matches 23; Conservative 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 95.0
Matches 19; Conservative
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
CCMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winharin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/774,954
FILING DATE: 30-Jan-2001
CLASSIFICATION NUMBER: US/08/978,741
RILING DATE: 26-NOV-1997
APPLICATION NUMBER: 08/792,498
FILING DATE: 31-JAN-1997
APTORNEY/AGENT: INFORMATION:
                                                                                                                ZIP: 94080
COMPUTER READABLE FORM:
MEDIUW TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFFWARE: Winbatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23 NOADHFLGSLAFAKLINRTLAVPPWIBYQHHKPPFTNLH 61
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Sequence 8, Application US/09774954
Sequence 8, Application No. US2004021645A1
GENERAL INFORMATION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA WAY
STREET: LONA WAY
STREET: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/774,954
FILING DATE: 30-Jan-2001
CLASSIFICATION: UNKNOWN>
PRIOR APPLICATION OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TILING DATE: 26-NOV-1997
APPLICATION NUMBER: US/08/978,741
FILING DATE: 31-JAN-1997
ATTORNEYS/ACENT INFORMATION:
NAME: SVODGGG CRAIG G.
REGISTRATION NUMBER: 39,044
FERERRENCE/DOCKET NUMBER: 91,041
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY: Linear SEQ ID NO: 17: US-09-774-954-17
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 343 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 8
US-09-774-954-8
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7

Gaps

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NETURE OF INVENTION: US/10424599

| Sequence 266118, Application US/10424599
| Publication No. US20040031072A1
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: La ROW Yibua
| APPLICANT: Cao Yongwei
| TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
| TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
| TITLE OF INVENTION: USADATE: US/10/424,599
| CURRENT FILING DATE: 2003-04-28
| WUMBER OF SEQ ID NOS: 285684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ä,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 152;
                                                                                                                                                                                                                                                                                                                             58 PKSRWDPAQKYLVYLPFEG-ISNQFYSFQNAATWAKRLNRTLVVXP 102
                                                                                                                                                                                         Query Match
24.4%; Score 86; DB 16; Length 110;
Best Local Similarity 47.8%; Pred. No. 0.0067;
Matches 22; Conservative 2; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                 2 PAGSWDPA-GYLLYCPCMGRFGNOADHFLGSLAFAKLLNRTLAVPP 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 22.8%; Score 80.5; DB 15; Length Best Local Similarity 41.9%; Pred. No. 0.049; Matches 18; Conservative 7; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 YLLYCPCMGRFGNQADHFLGSLAFAKLLNRTLAVPPWIEYOHH 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COTER INFORMATION: unsure at all Xaa locations FEATURE:
FEATURE:
CHER INFORMATION: Clone ID: PAT_MRT3847_82325C.1.pep US-10-424-599-266118
                  FEATURE:
NAME/KEY: unsure
LOCATION: (1). (110)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_61321C.1.pep
US-10-425-115-327031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Glycine max
ORGANISM: Zea mays
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LENGTH: 189
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT APPLICATION NUMBER: US/10/425,115
RUMBER OF SEQ ID NOS: 369326
SEQ ID NO 327031
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                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech) CURREY APPLICATION DATA:

APPLICATION NUMBER: US/09/774,954
FILING DATE: 30-Jan-2001
CLASSIPTCATION OF CURNOWN: APPLICATION NUMBER: US/08/978,741
FILING DATE: 26-NOV-1997
APPLICATION NUMBER: 08/792,498
FILING DATE: 31-JAN-1997
ATTORNEY/AGENT INFORMATION:
                                                                US-09-774-954-14

Sequence 14, Application US/09774954

Publication No. US20040241645A1

GENERAL INFORMATION:

APPLICANT: Yang Wang, Michael W. Spellman

TITLE OF INVENTION: O-Fucosyltransferase

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P1041P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; SEQUENCE DESCRIPTION: SEQ ID NO: 14: US-09-774-954-14
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; Sequence 327031, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                          CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO: 14:
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Sequence 113919
Sequence 113919 Application US/10437963
Shift and No. US20040123343A1
SERNERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Cao, Yorgwei
APPLICANT: Cao, Yorgwei
APPLICANT: Www. Wei
APPLICANT: Buckharov, Andrey A.
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22.0%; Score 77.5; DB 16; Length 538;
Best Local Similarity 44.2%; Pred. No. 0.47;
Matches 19; Conservative 4; Mismatches 17; Indels 3;
                                                                                                                                                                         Query Match 22.0%; Score 77.5; DB 16; Length 189; Best Local Similarity 45.5%; Pred. No. 0.15; Matches 20; Conservative 3; Mismatches 18; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                       10 GYLLYCPCMGRFGNQADHFLGSLAFAKLLNRTLAVPPWIEYQHH 53
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US-10-437-963-113919
                                                , OTHER INFORMATION: Clone ID: MRT4577_115198C.1.pep
US-10-425-115-201329
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Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: IKEDA, HARUO
APPLICANT: HORIKAMA, HINGSHI
APPLICANT: HORIKAMA, HINGSHI
APPLICANT: HORIKAMA, HINGSHI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REPRENCE: A49-262
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-274089
PRIOR PILLING DATE: 2001-05-30
PRIOR PILLING DATE: 2001-05-30
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 12551
TYPE: PRI
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ORGANISM: Oryza sativa
; FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
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1 MPAGSWDPAGYLLYCPCMGRFGNQADHFLGSLAFAKLLINRTLAVPPWIEYQHHKPPFTNL 60
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US-08-978-741-9
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Sequence 6, Appli
Sequence 7, Appli
Sequence 3, Appli
Sequence 5, Appli
Sequence 45921, A
Sequence 17, Appl
Sequence 13, Appli
Sequence 13, Appli
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14, Appl
14, Appl
3055, Ap
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5075, Ap
3610, Ap
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2, Appli
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6379, Ap
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Sequence 4, Appli
                                                                         October 25, 2005, 15:25:36; Search time 10.0205 Seconds (without alignments) 454.426 Million cell updates/sec
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Sequence 8
Sequence 1
Sequence 1
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Sequence
Sequence
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                                                                                                                                                     1 MPAGSWDPAGYLLYCPCMGR.....LAVPPWIEYQHHKPPFTNLH
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): /cgn2_6/ptodata1//iaa/6A_COMB.pep:*
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/ /cgn2_6/ptodata1//iaa/BECOMB.pep:*
): /cgn2_6/ptodata1//iaa/PCTUS_COMB.pep:*
): /cgn2_6/ptodata1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-08-978-741-14
US-09-33-729A-14
US-09-540-236-3055
US-09-578-592-5
US-09-18-111-5
US-09-640-211A-2258
US-09-589-110-5075
US-09-589-110-5075
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US-08-978-741-6
US-09-333-729A-7
US-08-978-741-3
US-09-333-729A-5
US-09-270-767-75
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US-09-543-681A-6379
US-09-902-540-16137
PCT-US91-00899-11
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US-08-978-741-8
                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                    513545 seqs, 74649064 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUMMARIES
                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                  OM protein - protein search, using sw model
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Maximum DB seq length: 200000000
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Match Length DB
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Perfect score:
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9626, Ap
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64, Appl
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Sequence 13, P
Sequence 12, P
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US-07-914-281-6

US-08-393-246-6

US-08-393-411-1

US-08-525-058A-6

US-08-395-800A-6

US-08-395-800A-10

US-08-395-800A-10

US-09-151-521-6

US-09-151-522-2

US-09-151-522-2

US-09-254-077A-11

US-09-254-077A-11

US-09-443-076-13

US-09-443-066-13

US-09-949-016-11353

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100.0%; Pred. No. 2.3e-40;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER REALANDLE FORM:

MEDIUM TYPES 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,741
FILING DATE: 26-No. 6100076-1997
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/792498
FILING DATE: 31
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                         Pagenene 9, Application US/08978741
Patent No. 6100076
GENERAL INFORMATION:
APPLICANT: Yang Wang, Michael W. Spellman
TITLE OF INVENTION: O-Fucosyltransferase
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetech, Inc.
                                                                                                                                                                                                                                   ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REPERENCE/POCKET NUMBER: P1041P1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                     STREET: 1 DNA WAY
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 61 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61; Conservative
   ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 incl
                                                                                                                                                                                                                                                                                                                                                                                    1 DNA Way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 61; Conserv
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1 MPAGSWDPAGYLLYCPCMGRFGNQADHFLGSLAFAKLLNRTLAVPPWIEYQHHKPPFTNL 60
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                                                                                                              Query Match 100.0%; Score 353; DB 3; Length 365; Best Local Similarity 100.0%; Pred. No. 2e-39; Matches 61; Conservative 0; Mismatches 0; Indels (
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US-08-978-741-6

Sequence 6, Application US/08978741

Patent No. 6100076

TITLE OF INVENTION:

TITLE OF INVENTION:

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE Geneticeh, Inc.

STREET: IDM WAY

STREET: IDM WAY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Wang, Yang
APPLICANT: Wang, Yang
APPLICANT: Spellman, Michael W.
TITLE OF INVENTION: O-FUCOSYL LEARSE
FILE REFERENCE: P1041P1D1-Substitute
CURRENT APPLICATION NUMBER: US/09/333,729A
CURRENT FILING DATE: 1999-06-15
PRIOR APPLICATION NUMBER: US 08/798,741
PRIOR PILING DATE: 1997-11-26
SEQ ID NO 3
SEQ ID NOS: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-333-729A-3; Sequence 3, Application US/09333729A; Sequent No. 62709B7; Patent No. 62709B7; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPITE: READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44
LENGTH: 365 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo Sapien
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US-08-978-741-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MPAGSWDPAGYLLYCPCMGRFGNQADHFLGSLAFAKLLNRTLAVPPWIEYQHHKRPFFTNL 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IMP PC hos/Ms-Dos
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,741
FILING DATE: 26-NO. 6100076-1997
CLASSIFFCATION: 435
PRIOR APPLICATION UMBER: 08/792498
APPLICATION NUMBER: 08/792498
APPLICATION NUMBER: 31
FILING DATE: 31
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | Sequence 2, Application US/08978741 |
| Patent No. 6100076 |
| Patent No. 6100076 |
| GENERAL INFORMATION: |
| APPLICANT: Yang Wang, Michael W. Spellman |
| TITLE OF INFORMATION: | O-Bucosyltransferase |
| TORRESPONDENCES: | TORRESPONDENCES: |
| CORRESPONDENCES: | O-Bucosyltransferase |
| STREET: | DNA Way |
| CITY: South San Francisco |
| STATE: California |
| COUNTRY: USA
                                                                                                                                     Sequence 4, Application US/09333729A

Patent No. 6270987

GENERAL INFORMATION:
GENERAL INFORMATION:
TILLE OF INVENTION:
FILE REFERENCE: 91041PlD1-Substitute
CURRENT APPLICATION NUMBER: US/09/333,729A

CURRENT PILING DATE: 1999-10-15

PRIOR PILING DATE: 1997-11-26

NUMBER OF SEQ ID NOS: 21

LENGTH: 61
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REFERENCE/DOCKET NUMBER: P10
TELECOMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
CORGANISM: Homo Sapien
US-09-333-729A-4
                    61 H 61
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; DB 3;
1.6e-32;
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PIBM PC compatible
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 295; DB; Pred. No. 1.6e-0; Mismatches
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APPLICANT: Spellman, Michael W.
TITLE OF INVENTION: O-Fucoayltransferase
FILE REFERENCE: P1041P1D1-Substitute
CURRENT APPLICATION NUMBER: US/09/333,729A
CURRENT FILING DATE: 1999-06-15
PRIOR PILING DATE: 1997-11-26
NUMBER OF SEQ ID NOS: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
IITLE OF INVENTION: O-Fucosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; LOCATION: 15, 17, 38
; OTHER INFORMATION: unknown amino acid
US-09-333-729A-5
                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,741
FILING DATE: 26-No. 6100076-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5, Application US/09333729A Patent No. 6270987 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 26-No. 6100076-12
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/792498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 650/225-1489
TELEPAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 91.5%;
Matches 54; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 91.5%;
Matches 54; Conservative
                                                                                                  Genentech, Inc
                                                                                                                                                            CITY: South San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 31
ATTORNEY/AGENT INFORMATION:
                                  NUMBER OF SEQUENCES: 1
                                                                                                                                 1 DNA Way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: Amino Acid
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: unsure
LOCATION: 15, 17
                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-333-729A-5
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                                                                                                                                 STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MPAGSWDPAGYLLYCPCMGRFGNQADHFLGSLAFAKLINRTLAVPPWIEYQHHKPPFTNL 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 353; DB 3; Length 397;
Pred. No. 2.2e-39;
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US-09-333-729A-7
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Pred. No. 2.2e-39;
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Patent No. 6100076
GENERAL INFORMATION:
APPLICANT: Yang Wang, Michael W. Spellman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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APPLICANT: Spellman, Michael W.
TITLE OF INVENTION: O-PROGRYLTRANSFERAGE
FILE REFERENCE: P1041P1D1-Substitute
CURRENT APPLICATION NUMBER: US/09/333, 729A
CURRENT FILING DATE: 1999-06-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR PAPLICATION NUMBER: US 08/798,741
PRIOR PILING DATE: 1997-11-24
NUMBER OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANSPORTED OF THE TRANS
          26-No. 6100076-1997
N: 435
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                                                                                                                             FILING DATE: 31
ATTORNEY/AGENT INFORMATION:
NAME: SVODOMA, CTAIG G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P104:
TELECOMUNICATION INFORMATION:
TELEPHONE: 650/252-1489
TELEFAX: 650/252-1489
TELEFAX: 650/252-1881
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTREISTICS:
                                        CLASSIPICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/792498
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Best Local Similarity 100.0%;
Matches 61; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 397 amino acids
Amino Acid
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Best Local Similarity 100.
Matches 61; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  H 93
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LENGTH: 397
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Score 295; DB 3; Length 61;
Pred. No. 1.6e-32;
                                                5; Indels
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0; Gaps

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Length 343;
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US-08-978-71-8

Sequence 8, Application US/08978741

Patent No. 6100076

GENERAL INFORMATION:
TITLE OF INVENTION: Michael W. Spellman
TITLE OF INVENTION: O-FUCOSYltransferase
NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:
ADDRESSE: Genentech, Inc.
STREET: 1 DNA Way
COUNTRY: California
COUNTRY: California
COUNTRY: USA

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,741
FILING DATE: 26.No. 6100076-1997
CLASSIFICATION NUMBER: 08/792498
FILING DATE: 31
ATTORNEY/AGENT INFORMATION:
NAME: SOADCA, CRANGE
REFERENCE/DOCKET NUMBER: 39,044
REFERENCE/DOCKET NUMBER: 91041P1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 650/252-1489
                                                                                                                                       61
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61.8%; Score 218; DB 3; I
Best Local Similarity 100.0%; Pred. No. 3.4e-21;
Matches 39; Conservative 0; Mismatches 0;
Best Local Similarity 100.0%; Pred. No. 3.4e-21; Matches 39; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                          US-00-333-729A-13
Sequence 13, Application US/09333729A
Patent No. 6270987
GENERAL INFORMATION:
APPLICANT: Wangy Yan
APLICANT: Spellman, Michael W.
TITLE OF INVENTION: O-PLOCSYLtransferase
FILE REFERENCE: P1041P1D1-Substitute
CURRENT FILING DATE: 1999-06-15
PRIOR APPLICATION NUMBER: US 08/798,741
PRIOR FILING DATE: 1997-11-26
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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SEQ ID NO 13
LENGTH: 343
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CORGANISM: Homo Sapien
US-09-333-729A-13
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US-09-270-767-45921
Sequence 45921, Application US/09270767
Fatent No. 6701491
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
TITLE OF INVENTION: Number: US/09/270,767
CURRENT APPLICATION NUMBER: US/09/270,767
NUMBER OF SEQ ID NOS: 62517
SOFTWARE PATENTIN Ver. 2.0
SOFTWARE PATENTIN Ver. 2.0
SEQ ID NO 45921
          3 AGSWDLAGYLLYXPXMGRFGNQADHFLGSLAFAKLXVRTLAVPPWIEYQHHKPPFTNLH 61
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: 1BM PC COMPATION: 1.44 Mb floppy disk COMPUTER: 1BM PC COMPATION: 1.44 Mb floppy disk COMPUTER: 1BM PC COMPATION: 1.44 Mb floppy disk OFFERTING SYSTEM: PC-DOS/MS-DOS OFFETATION SYSTEM: PC-DOS/MS-DOS OFFETATION NUMBER: US/OS/9792498
FILING DATE: 3.6 ND. 610076-1997
CLASSIFICATION DATA: APPLICATION NUMBER: 08/792498
FILING DATE: 31
ATTORNEY/AGENT INFORMATION:
NAME: SYDAGMA CTAIG G.
RESTRENCE/DOCKET NUMBER: 39,044
RESTRENCE/DOCKET NUMBER: 91041P1
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Drosophila melanogaster
US-09-270-767-45921
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SEQUENCE CHARACTERISTICS:
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Amino Acid
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US-08-978-741-17
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Gaps

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US-09-333-729A-14
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                                                                                               Score 123; DB 3; Length 474;
Pred. No. 3.6e-08;
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                                                                                                                                       Indels
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COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech) CURRENT APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US/08/978,741 FILING DATE: 26-No. 6100076-1997 CLASSIFICATION: 435 PRIOR APPLICATION NUMBER: 08/792498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
34.8%; Score 123; DB 3;
Best Local Similarity 67.6%; Pred. No. 3.6e-08;
Matches 23; Conservative 5; Mismatches 6
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                                                                                                                                                                              19 GRFGNQADHFLGSLAFAKLLNRTLAVPPWIEYQH 52
                                                                                                                                                                                                                                                                            RESULT 13
US-09-333-729A-12
Sequence 12, Application US/09333729A
Sequence 12, Application US/09333729A
RENERAL INFORMATION:
APPLICANT: Wang, Yang
APPLICANT: Spellman, Michael W.
TITLE OF INVENTION: O-Fucosyltransferase
FILE REFERENCE: P1041P1D1-Substitute
CURRENT PELLING DATE: 1999-06-15
PRIOR PELLING DATE: 1999-06-15
PRIOR PILING DATE: 1999-11-26
NUMBER OF SEQ ID NOS: 21
SEQ ID NO 12
LENGTH: 474
TYPE: PRT
ORGANISM: Caenorhabditis Elegans
                                                                                                                                       5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 14, Application US/08978741
Patent No. 610076
GENERAL INFORMATION:
APPLICANT: Yang Wang, Michael W. Spellman TITLE OF INVENTION: 0-Fucosyltransferase NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 31
ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Genentech, Inc. STREET: 1 DNA Way CITY: South San Francisco STATE: California COUNTRY: USA
                                                                                             Query Match
Best Local Similarity 67.6%;
Matches 23; Conservative 5
LENGTH: 474 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-333-729A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 14
US-08-978-741-14
                                                          US-08-978-741-8
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                                                                                                                                                                                                                                       Query Match
28.6%; Score 101; DB 3; Length 28;
Best Local Similarity 90.0%; Pred. No. 1.1e-06;
Matches 18; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
CTHER INFORMATION: Plasmid insert encoded protein.
NAME/KEY: unsure
COCATION: 23, 25
COTHER INFORMATION: unknown amino acid
US-09-333-729A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 101; DB 3;
Pred. No. 1.1e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Wang, Yang
APPLICANT: Wang, Yang
APPLICANT: Spellman, Michael W.
TITLE OF INVENTION: O-Fucosyltransferase;
FILE REFERENCE: P1041P1D1-Substitute
CURRENT APPLICATION NUMBER: US/09/333,729A
CURRENT FILING DATE: 1999-06-15
PRIOR APPLICATION NUMBER: US 08/798,741
PRIOR FILING DATE: 1997-11-26
NUMBER OF SEQ ID NOS: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Search completed: October 25, 2005, 15:42:49 Job time : 11.0205 secs
REFERENCE/DOCKET NUMBER: P1041P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 14, Application US/09333729A Patent No. 6270987
                                                                                                                                                                                                                                                                                                                                      1 MPAGSWDPAGYLLYCPCMGR 20
                                                                                                                                                                                                                                                                                                                                                                9 MPAGSWDPAGYLLYXPXMGR 28
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                                  TELEPHONE: 650/225-1489
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: Amino Acid
                  TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
TELEFAX: 650/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28.6%;
90.0%;
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 28.6
Best Local Similarity 90.0
Matches 18; Conservative
                                                                                                                                                                           TOPOLOGY: Linear
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OLASO MANA BARA (USETO)

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October 25, 2005, 15:20:23; Search time 38.8296 Seconds (without alignments) 607.588 Million cell updates/sec
                                                                                                                                                                                                                        61
                                                                                                                                                                                                                        1 MPAGSWDPAGYLLYCPCMGR.....LAVPPWIEYQHHKPPFTNLH
                                                                                                                                                                                                                                                                                                                                                        2105692
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                     2105692 segs, 386760381 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                     - protein search, using sw model
                                                                                                                                                                                                                                                               BLOSUM62
Gapop 10.0 , Gapext 0.5
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geneseqp2003as:*
geneseqp2003bs:*
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geneseqp1980s:*
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Maximum DB seq length: 200000000
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353
                                                                                                                                                                                     Title:
Perfect score:
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                                                                           OM protein
                                                                                                                                                                                                                            Sequence:
                                                                                                                                                                                                                                                                                                                   Searched:
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                                                                                                              Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Aaw80574 N-termina	Aaw80571 Human hea	Abm82223 Tumour-as					0					•	Abm69163 Photorhab		Adl05369 M. catarr			Aab33303 Pinus rad		Abu01274 S. pneumo			Aau38005 Streptoco	Abu45987 Protein e
SUMMARIES	ΙD	AAW80574	AAW80571	ABM82223	AAW80573	AAW80572	AAM78377	AAM79361	ABB63790	AAW80577	AAY87325	AAW80575	ABB97437	ABU35781	ABM69163	ABU34983	ADL05369	ADN25627	AAR63066	AAB33303	ADK48560	ABU01274	ADR94975	AAU37750	AAU38005	ABU45987
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	* Query Match Length	61	365	388	397	61	417	417	402	343	150	28	1561	223	366	191	205	580	340	412	737	741	763	767	767	767
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	% Query Match	100.0	100.0	100.0	100.0	83	9	9	63	6	34	28	5	Ŧ	ਜ	ä	ដ	ដ	H	H	H	Η	H	17	H	H
	Score	353	353	353	353	295	241.5	229.5	223	218	120	101	69.5	64.5	64	63.5	63.5	63.5	62.5	62	60.5	60.5	60.5	60.5	60.5	60.5
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This represents a the N-terminal sequence of the human heart Offucosyltransferase that can glycosylate an epidermal growth factor (EGF) domain of a polypeptide with an activated O-fucose residue. Inhibitors of O-fucosyltransferase, e.g. mutants with increased affinity for the EFG domains, are used in diagnosis and treatment of conditions associated with overexpression of O-fucosyltransferase, to promote survival of sensory (retinal) neurons. Probes based on EGF domain polypeptide are used to detect gene amplification and expression. The expression can also be determined at the protein level using antibodies specific for O-

fucosyltransferase Sequence 61 AA;

Aay81596 Streptoco	Aaw97416 A membran	Abu36823 Protein e	Abu34438 Protein e	Abu33866 Protein e	Aay91094 Human G p	Aau08997 Human G p	Aae03544 Human G-p	Aam51415 Human OT7	Abb79864 Human G-p	Abp97222 Tumour-as	Abp81995 Human G p	Adn39505 Cancer/an	Adn39430 Cancer/an	Adg19755 Human G p	Adl91585 Human imm	Ado29412 Human GPC	Adq89080 Human uro	Adr21325 Human met	Adt05941 Human OT7
AAY81596	AAW97416	ABU36823	ABU34438	ABU33866	AAY91094	AAU08997	AAE03544	AAM51415	ABB79864	ABP97222	ABP81995	ADN39505	ADN39430	ADG19755	ADL91585	AD029412	ADQ89080	ADR21325	ADT05941
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16	78	19	19	19	39	39	398	39	39	39	39	39	39	39	39	39	39	39	39
-		0	0	6	0	6.9	16.9	σ.	16.9	0.	16.9	6	6	σ.	6	6	0	6.9	6.
17	17	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16
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26	27	28	5	30	- E	35	33	34	35	36	37	38	99	40	41	4	4 .	44	45

ALIGNMENTS

Human O-fucosyl:transferase able to glycosylate epidermal growth factor domains - useful for diagnosis and treatment of diseases involving overexpression of the enzyme. N-terminal amino acid sequence of human heart O-fucosyltransferase O-fucosyltransferase; epidermal growth factor; EGF; glycosylation; O-fucose; inhibitor; sensory neuron; retinal neuron; human; heart. Ā Claim 4; Page 69; 90pp; English. AAW80574 standard; peptide; 61 97WO-US023401. 97US-00792498. 97US-00978741. (first entry) (GETH) GENENTECH INC. Wang Y, Spellman MW; WPI; 1998-437477/37. Homo sapiens. WO9833924-A1. 17-DEC-1997; 31-JAN-1997; 26-NOV-1997; 16-DEC-1998 06-AUG-1998 AAW80574; RESULT 1 AAW80574

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1 MPAGSWDPAGYLLYCPCMGRFGNQADHFLGSLAFAKLLNRTLAVPPWIEYQHHKPPFTNL 60
                                   61 H 61
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                                                                                                                      RESULT 3
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                                                                                                     1 MPAGSWDPAGYLLYCPCMGRFGNQADHFLGSLAFAKLINRTLAVPPWIEYQHHKPPFTNL
                                                                                    1 MPAGSWDPAGYLLYCPCMGRFGNQADHFLGSLAFAKLLNRTLAVPPWIEYQHHKPPFTNL
                                                    Gaps

    .61
    /note= "N-terminal sequence claimed for in claim 4"

                                                                                                                                                                                                                                                                                                                                                                                                     O-fucosyltransferase, epidermal growth factor, EGF, glycosylation, O-fucose, inhibitor, sensory neuron, retinal neuron, human, heart.
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                    Length 61;
                  Query Match
100.0%; Score 353; DB 2; Length 6:
Best Local Similarity 100.0%; Pred. No. 4.8e-40;
Matches 61; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 100.0%; Score 353; DB 2; Similarity 100.0%; Pred. No. 3.8e-39; 61; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                     AAW80571 standard; protein; 365 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Fig 12A; 90pp; English.
                                                                                                                                                                                                                                                                                                                                                                      Human heart O-fucosyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97WO-US023401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97US-00792498
97US-00978741
                                                                                                                                                                                                                                                                                                                                     16-DEC-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Spellman MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1998-437477/37.
N-PSDB; AAV65632.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 365 AA;
                                                                                                                                                    61 H 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9833924-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-AUG-1998.
                                                                                                                                                                                                                                                                                                     AAW80571;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wang Y,
                                                                                                                                                                                                                                       RESULT 2
                                                                                                                                                                                                                                                                                        %XCCCCCCCX8X144X88X6X8X88X6X9X8X143X8X4X6XXX
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The invention relates to human tumour-associated antigenic target (TAT) polypeptides are polypeptides are polypeptides are overexpressed in cancer tissues compared to normal tissues, and may thus serve as effective targets for the diagnosis and treatment of cancer in ammanls. The invention also relates to nucleic acid and polypeptide mannals. The invention also relates to nucleic acids and compressed on polypeptides arguession vectors and host cells comprising a TAT nucleic acid; an antibody specific for a TAT polypeptide; dead on proteins comprising a nucleic acid; an antibody specific for a TAT polypeptide; nucleic acid; and methods and compositions for the treatment or diagnosis of cancer in mammals. TAT polypeptides, nucleic acids, antibodies, antagonists, binding molecules and compositions are useful for diagnosis of treating a cell proliferative disorder associated with increased TAT expression, particularly cancers such as breast cancer, lung cancer, lung cancer, cancer, such as breast cancer, colorectal cancer, lung cancer, or cancer, such as breast cancer, concerned and leukaemia. TAT nucleic acids may further be nervous system, melanoma and leukaemia. TAT nucleic acids may further be chromosome identification and in gene therapy. The present sequence
                                                                                                                                                                                                                                   Tumour-associated antigenic target (TAT) polypeptide PRO83146, SEQ:5726.
                                                                                                                                                                                                                                                                       Tumour-associated antigenic target; TAT; human; overexpression; cancer; tumour; diagnosis; cell proliferative disorder; breast cancer; colorectal cancer; lung cancer; ovarian cancer; liver cancer; central nervous system cancer; bladder cancer; pancreatic cancer; certical cancer; melanoma; leukaemia; hybridisation probe; chromosome identification; chromosome mapping; gene mapping; gene therapy; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New tumor-associated antigenic target polypeptides and nucleic acids, useful in preparing a medicament for treating or detecting a proliferative disorder, e.g. breast, lung, colorectal, ovarian or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 353; DB 8; Length 388;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 12; SEQ ID NO 5726; 7273pp; English.
                                                                                                           ABM82223 standard; protein; 388 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-SEP-2003; 2003WO-US028547.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-OCT-2002; 2002US-0414971P.
                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   prostate cancer or tumor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; ACN40746.
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61 H 61
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                                                                                                                                                                                             18-NOV-2004
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Gaps

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0; Indels

Matches

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1 MPAGSWDPAGYLLYCPCMGRFGNQADHPLGSLAFAKLLNRTLAVPPWIEYQHHKPPFTNL

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-11
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                                                                                                                       AAW80572
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
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                                                                                RESULT 5
                                                                                        AAW80572
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fucosyltransferase expressed by a plasmid insertion. The human Offucosyltransferase can glycosylate an epidermal growth factor (EGF) fucosyltransferase can glycosylate an epidermal growth factor (EGF) of placesyltransferase, e.g. metants with increased affinity for the EFG domains, are used in diagnosis and treatment of conditions associated with overexpression of Oftucosyltransferase, to promote survival of sensory (retinal) neurons. Probes based on EGF domain polypeptide are used to detect gene amplification and expression. The expression can also be determined at the protein level using antibodies specific for Oftucosyltransferase.
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                                         24 MPAGSWDPAGYLLYCPCMGRFGNQADHFLGSLAFAKLLNRTLAVPPWIEYQHHKPPFTNL 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human O-fucosyl:transferase able to glycosylate epidermal growth factor domains - useful for diagnosis and treatment of diseases involving
                             1 MPAGSWDPAGYLLYCPCMGRFGNQADHFLGSLAFAKLLNRTLAVPPWIEYQHHKPPFTNL
                                                                                                                                                                                                            Human O-fucosyltransferase sequence expressed by a plasmid insertion
         Gaps
                                                                                                                                                                                                                               O-fucosyltransferase; epidermal growth factor; EGF; glycosylation; O-fucose; inhibitor; sensory neuron; retinal neuron; human; heart.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This represents the amino acid sequence of the human heart O-
fucosyltransferase expressed by a plasmid insertion. The human O-
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         Indels
100.0%; Pred. No. 4.1e-39; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                           27. .32
/note= "polyhistidine tag"
                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                AAW80573 standard; protein; 397 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example; Fig 13B; 90pp; English
                                                                                                                                                                                                                                                                                                                                                                                                       97US-00792498.
97US-00978741.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  overexpression of the enzyme
                                                                                                                                                                                                                                                                                                                                                                                    97WO-US023401
                                                                                                                                                                                         (first entry)
            61; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Spellman MW;
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  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAV65633
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26-NOV-1997;
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                                                                                                                                                                                                                                                                               Synthetic
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                                                                                                                                                                     AAW80573;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wang Y,
   Best Local
                                                                                                                                                                                                                                                                                                           Peptide
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            Matches
                                                                                                                                        AAW80573
                                                                                                                            RESULT
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with overexpression of O-fucosyltransferase, to promote survival of sensory (retinal) neurons. Probes based on EGF domain polypeptide are used to detect gene amplification and expression. The expression can also be determined at the protein level using antibodies specific for O-
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33 MPAGSWDPAGYLLYCPCMGRFGNQADHFLGSLAFAKLLNRTLAVPPWIEYQHHKPPFTNL 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human O-fucosyl:transferase able to glycosylate epidermal growth factor domains - useful for diagnosis and treatment of diseases involving
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This represents the N-terminal sequence of CHO O-fucosyltransferase. I enzyme can glycosylate an epidermal growth factor (EGF) domain of a polypeptide with an activated O-fucose residue. Inhibitors of O-fucose residue. Inhibitors of O-fucose and the properties of O-fucose and treatment of conditions associated with overexpression of O-fucosyltransferase. Lo promote survival of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                        O-fucosyltransferase; epidermal growth factor; EGF; glycosylation;
O-fucose; inhibitor; sensory neuron; retinal neuron; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                               N-terminal amino acid sequence of CHO O-fucosyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 295; DB 2; I
Pred. No. 3.8e-32;
0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                               AAW80572 standard; peptide; 61 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note= "unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 5; Page 69; 90pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note= "unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "unknown"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         overexpression of the enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 83.6%;
1 Similarity 91.5%;
54; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97US-00792498.
                                                                                                                                                                                                                                                                                                                                        16-DEC-1998 (first entry)
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                                                                                  H 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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Conservative

Local Similarity hes 61; Conserv

Best Loca Matches

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Gaps

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AAM79361 standard; protein; 417 AA.

AAM79361 ID AAM7

(first entry)

06-NOV-2001

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The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (KAAF9323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides have various cytokine-like activity esem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, haematopoiesis regulating activity tissue growth factor activity, immunomodulatory activity and activity, tissue growth factor activity, immunomodulatory activity and activity, insupposed activity and activity in activity and solvent of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80202) are omitted as the relevant pages from the sequence listing were missing at the time of publication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy.
                                                                                                                                                                                  Human, cytokine, cell proliferation, cell differentiation, gene therapy, vaccine, peptide therapy, stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory, cancer, leukaemia; nervous system disorder; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y; Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW; Xue AJ, Yang Y, Wejhrman T, Goodrich R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 20; Page 3276-3277; 6221pp; English.
                                 AAM78377 standard; protein; 417 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-APR-2000; 2000US-00560875.
20-UTW-2000; 2000US-00598075.
19-UTL-2000; 2000US-0063325.
01-SEP-2000; 2000US-00654936.
15-SEP-2000; 2000US-0065351.
20-CCT-2000; 2000US-0063325.
                                                                                                                                              Human protein SEQ ID NO 1039.
                                                                                                                                                                                                                                                                                                                                                                                              05-FEB-2001; 2001WO-US004098
                                                                                                                                                                                                                                                                                                                                                                                                                                  03-FEB-2000; 2000US-00496914
                                                                                                            06-NOV-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                      WO200157190-A2
                                                                                                                                                                                                                                                                                    Homo sapiens.
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                                                                      AAM78377;
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RESULT 6
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ABB63790
ID ABB63790 standard; protein; 402 AA.
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                                                                                                                 7 DPAGYLLYCPCM----GRFGNQADHFLGSLAFAKLINRTLAVPPWIEYQHHKPPFTNLH 61
                                             5; Gaps
/ Match 68.4%; Score 241.5; DB 4; Length 417; Local Similarity 76.7%; Pred. No. 6.8e-24; les 46; Conservative 3; Mismatches 6; Indels 5;
                          Best Loca
Matches
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RESULT 7

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The invention relates to polymucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polymucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoissis regulating activity, tissue growth factor activity, immunomodulatory activity and activity, inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111 sequence listing were missing at the time of publication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54 DMATWPTHAPSVEEGGGGRFGNQADHFLGSLAFAKLLNRSLAVPSWIEYQHHKPPFTNLH 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                              Human, cytokine, cell proliferation, cell differentiation, gene therapy, vaccine, peptide therapy; stem cell growth factor; haematopolesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 DPAGYLLYCPCM----GRFGNQADHFLGSLAFAKLLNRTLAVPPWIEYQHHKPPFTNLH
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Chen R, Wang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Liu C, Drmanac RT, Asundi V, Zhou P, Xi
ao QA, Wang D, Wang J, Zhang J, Ren F,
Yang Y, Wejhrman T, Goodrich R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 20; Page 229-230; 6221pp; English.
                                                                                                                                                                                                                                                                                                                                   03-FBB-2000; 2000US-00496914.
27-AFR-2000; 2000US-00560875.
20-UNA-2000; 2000US-00598075.
19-UUL-2000; 2000US-00598075.
15-SBP-2000; 2000US-00654936.
15-SBP-2000; 2000US-00663325.
30-NOV-2000; 2000US-0069325.
                                                                               Human protein SEQ ID NO 3007.
                                                                                                                                                                                                                                                                                                    05-FEB-2001; 2001WO-US004098
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Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HYSE-) HYSEQ INC.
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                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tang YT, Li
Ma Y, Zhao
                                                                                                                                                                                                                                                                      09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44;
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Matches
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This represents a published partial human sequence of unknown function from a myeblast cell line. The invention provides a human heart Ofucosyltransferase enzyme that can glycosylate an epidermal growth factor (EGF) domain of a polypeptide with an activated O-fucose residue. Inhibitors of O-fucosyltransferase, e.g. mutants with increased affinity for the EFG domains, are used in diagnosis and treatment of conditions associated with overexpression of O-fucosyltransferase, to promote survival of sensory (retinal) neurons. Probes based on EGF domain polypeptide are used to detect gene amplification and expression. The expression can also be determined at the protein level using antibodies specific for O-fucosyltransferase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia; asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia; Parkinson's disease; Huntington's diseases; ovulatory defect;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Human O-fucosyl:transferase able to glycosylate epidermal growth factor domains - useful for diagnosis and treatment of diseases involving
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human signal peptide containing protein HSPP-102 SEQ ID NO:102.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 61.8%; Score 218; DB 2; Length 343; Sest Local Similarity 100.0%; Pred. No. 8.6e-21; Atches 39; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 NQADHFLGSLAFAKLLNRTLAVPWIEYQHHKPPFTNLH 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23 NOADHFLGSLAFAKLLNRTLAVPPWIEYQHHKPPFTNLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Page 62-68; 90pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY87325 standard; protein; 150 AA
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98US-0094983P.
                                                                                                                           97US-00792498.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               overexpression of the enzyme.
                                                            97WO-US023401.
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                                                                                                                                                                                                                         (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                      Spellman MW;
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31-JUL-1998;
                                                               17-DEC-1997;
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06-AUG-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLi6176-ABL30511), expressed DNA ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Partial human seguence of unknown function from a myeblast cell line.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          O-fucosyltransferase; epidermal growth factor; EGF; glycosylation; O-fucose; inhibitor; sensory neuron; retinal neuron; human; heart.
                                                                                                                                                                                                                             Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 18162; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 402;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28 DPNGYLTYCPCMGRFGNQADHFLGSLAFAKALNRTLILPPWVEYR 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 DPAGYLLYCPCMGRFGNQADHFLGSLAFAKLLNRTLAVPPWIEYQ 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                             melanogaster polypeptide SEQ ID NO 18162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 223; DB 4;
Pred. No. 2.2e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW80577 standard; protein; 343 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Li PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-MAR-2001; 2001WO-US009231.
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84.4%;
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11-JUL-2000; 2000US-00614150.
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Best Local Similarity 84.4
Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster.
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N-PSDB; ABL07893.
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                                                                                                                                                                                                                                                                        pharmaceutical
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                                                                                                    26-MAR-2002
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RESULT 9 **AAW80577**

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                                                                                                                                                                               New human signal peptide-containing proteins useful in treatment, prevention and diagnosis of e.g. cancer, inflammation and cardiovascular disease.
                                                                         Lal P, Tang YT, Gorgone GA, Corley NC, Guegler KJ, Baughn MR;
Akerblom IE, Au-Young J, Yue H, Patterson C, Reddy R, Hillman JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              O-fucosyltransferase, epidermal growth factor; EGF; glycosylation; O-fucose; inhibitor; sensory neuron; retinal neuron; human; heart.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-terminal sequence of expressed human O-fucosyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 34.0%; Score 120; DB 3; Length 150; Best Local Similarity 95.0%; Pred. No. 7.3e-08; Matches 19; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                           Claim 1; Page 225-226; 327pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW80575 standard; protein; 28 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MPAGSWDPAGYLLYCPCMGR 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "unknown
98US-0102686P.
98US-0112129P.
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                                             (INCY-) INCYTE PHARM INC.
                                                                                                                                       WPI; 2000-160673/14.
N-PSDB; AAZ98210.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seguence 150 AA;
01-OCT-1998;
11-DEC-1998;
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Synthetic.
                                                                                                         Bandman O;
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This represents the N-terminal amino acid sequence of the human heart O-fucosyltransferase expressed by a plasmid insertion. The human O-fucosyltransferase can glycosylate an epidermal growth factor (EGF) domain of a polypeptide with an activated O-fucose residue. Inhibitors of O-fucosyltransferase, e.g. mutants with increased affinity for the EFG domains, are used in diagnosis and treatment of conditions associated with overexpression of O-fucosyltransferase, to promote survival of sensory (retinal) neurons. Probes based on EGF domain polypeptide are used to detect gene amplification and expression. The expression can also be determined at the protein level using antibodies specific for O-fucosyltransferase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human O-fucosyl:transferase able to glycosylate epidermal growth factor domains - useful for diagnosis and treatment of diseases involving overexpression of the enzyme.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABB97437 standard; protein; 1561 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Page 39; 90pp; English.
Misc-difference 25
/note= "unknown"
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97US-00978741
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nes 18; Conservative
                                                                                                                                                                                                                                                                                                                                                         (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                  Spellman MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1998-437477/37.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 28 AA;
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                                                                                                                                                                                                                                                                     31-JAN-1997;
26-NOV-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                           Wang Y,
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Matches
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                                                                                                                                                                 The present invention provides the protein and coding sequences of 444 novel human proteins. These were isolated from expressed sequences tags (ESTs). They can be used to stimulate call growth, to regulate haematopoiesis e.g. to treat aplastic anamaia, to help tissue regrowth e.g. in burn treatment, to regulate the immune system e.g. to treat multiple sclerosis, to regulate activin or inhibin e.g. to treat infertility, to regulate haemostasis or thrombolysis e.g. to treat and cancer, to screen for drugs, to treat inflammatory conditions e.g. rheumatoid arthritis, and to treat nervous system disorders e.g. Parkinson's disease. The present sequence is a protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antisense; prokaryotic essential gene; cell proliferation; drug design.
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1342 TWEQGRYLLWNPCSGHFYGQFD-----TFCPLKNVGCLIGPDNIWFNIQRYESP 1390
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Xu HH;
                                                                                             An isolated polynucleotide for treating diseases associated with its encoded polypeptide such as cancer and multiple sclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                     5 SWDPAGYLLYCPCMGRFGNQADHFLGSLAFAKLLNRTLAVPP---WIEYQHHKPP 56
         Ren F;
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                                                                                                                                                                                                                                                                                                                                                              Score 69.5; DB 5; Length 1561;
Pred. No. 8.4;
                                                                                                                                                                                                                                                                                                                                                                                          7; Mismatches 23; Indels
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Forsyth RA,
         Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein encoded by Prokaryotic essential gene #21308.
       Zhou P, Asundi V, Zhang J,
Wehrman T, Drmanac RT;
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Yamamoto R,
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                                                                                                                                         Claim 20; SEQ ID NO 705; 509pp; English
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Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2001US-00948993.
2001US-0342923P.
2002US-00072851.
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                                                                                                                                                                                                                                                                                                                                                              19.7%;
ilarity 29.1%;
Conservative
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Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium leprae.
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N-PSDB; ACA39651.
                                                     2002-292408/33
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nes 16; Conserv
          Liu C,
Yang Y,
                                                                                                                                                                                                                                                                                                                                    Sequence 1561 AA;
                                                                   N-PSDB; ABN32623
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08-FEB-2002;
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          Tang YT,
Xue AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABU35781;
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Matches
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Wall
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the first antisense sequences given in the specification where expression the fell antisense sequences given in the specification where expression of the muclaic acid inhibites proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular colferation or that that an an operon required for proliferation or that has an activity against a biological pathway the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a compound that inhibits proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound, a activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent compound, a activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent compound; a confideration to isolate candidate molecules for rational drug discovery programs, or for screening for homologous nucleic acids are useful for for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. arruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence acid acid or this enterty from Interest for the proliferation in electronic format direct
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antibacterial; fungicide; insecticide; polymorphism; genetic analysis; detection; food; gene expression; plant; animal; microorganism; toxin; antibiotic; biopesticide; virulence factor; disease model; plague;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Photorhabdus luminescens protein sequence #2260.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 FGNQADHFLGSLAFAKLLNRTLAV---PPWIE 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABM69163 standard; protein; 366 AA
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(CNRS ) CNRS CENT NAT RECH SCI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-NOV-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Photorhabdus luminescens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 223 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                whooping cough
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200294867-A2
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Danchin A;

Duchaud E, Taourit S, Glaser P, Frangeul L, Kunst F,

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The invention relates to the isolation of genes and their encoded proteins from Photorhabdus luminescens. The isolated sequences are sources of probes and primers for detecting the geneme of P. Luminescens and related species; to study polymorphisms; for gene analysis and for detection/amplification of the genes. Antibodies (Ab) raised against the polypeptides encoded by the genes are used for detection/identification of P. Luminescens, e.g. in foods. The genes, proteins, Ab and cells that carry a gene-containing vector are used for detection/identification of P. Luminescens, e.g. in foods. The genes, proteins, Ab and cells that carry a gene-containing vector are used to select compounds that capture, regulate, induce or inhibit expression of the genes in plants, animals or microorganisms other than P. luminescens and are able to alter response or sensitivity to toxins and antibiotics produced by P. Luminescens. Cells transformed to express the genes are useful for recombinant production of the proteins, particularly toxins and cantibacterials useful as insecticides, bactericides and fungicides. The genes, proteins, vectors containing the genes and Ab are also useful therapeutically (to treat microbial infection by bacteria or fungi that are sensitive to P. luminescens encoded toxins or antibiotics) and as biopesticides. Other uses of the genes and the proteins are as virulence factors and for identifying targets of human diseases for which P. Luminescens is a model (particularly plague and whooping cough). This sequence represents one of the isolated P. luminescens proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 SWDPAGYLLYCPCMGRFGNQADHFLGSLAFAKLLNRTLAV--------PPWI 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                    Genomic sequence of Photorhabdus luminescens and encoded polypeptides, useful e.g. as therapeutic antimicrobials and agricultural pesticides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match

Quert Local Similarity 18.1%; Score 64; DB 6; Length 366;

Quert Local Similarity 33.3%; Pred; No. 8.7; I andels
Matches 21; Conservative 6; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein encoded by Prokaryotic essential gene #20510.
                                                                                                                                                   Claim 2; SEQ ID NO 2260; 1205pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABU34983 standard; protein; 191 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-MAR-2002; 2002WO-US009107.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-MAR-2001, 2001US-00815242.
06-SEP-2001, 2001US-00948993.
25-OCT-2001, 2001US-0342923P.
08-FEB-2002, 2002US-0362699P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Moraxella catarrhalis.
                                          WPI; 2003-148459/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 366 AA;
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the fall antisence for an isolated nutter and comprising any one of the nucleic acid inhibite proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation or the activity of a gene in an operon required for proliferation, or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation of the biological pathway in which a proliferation required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profilling a compound activity, (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent product lead to the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism and organism acts order are useful for proliferation of an organism or some organism and organism and organism. The antisense nucleic acids required for cellular proliferation to isolate molecules for actional
                                                                                                                                                                      New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                              The invention relates to an isolated nucleic acid comprising any one of
                 Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25 ADH-----FLGSLAFAKLLNRTLAVPPWI----EYQHHK--PPFTNL 60
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                       Ohlsen KL,
Forsyth RA,
                       Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                              Claim 25; SEQ ID NO 62907; 1766pp; English.
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                       Malone C,
Carr GJ,
                       Zamudio C,
Trawick JD,
                                                                                                  2003-029926/02.
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Les 19; Conserv
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Best Local Si
Matches 199
                       Wang L,
Wall D,
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